

SEQUENCE LISTING

<110> Bejanin, Stephan  
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

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<150> 2001-08-10

<151> 60/311,305

<150> 2001-08-24

<151> 60/314,734

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<151> 60/318,204

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Val Ile Ser Cys Ala Lys Asp Gly Val Lys Phe Ser Ala Ser Gly Glu
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55          60          65
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Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr Lys Ala Thr Pro Leu Ser
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Ser Thr Val Thr Leu Ser Met Ser Ala Asp Val Pro Leu Val Val Glu
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Tyr Lys Ile Ala Asp Met Gly His Leu Lys Tyr Tyr Leu Ala Pro Lys
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Ile Glu Asp Glu Glu Gly Ser
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 Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn Glu Pro  
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 Thr Leu Asn Ile Lys Thr Arg Lys Pro Ala Leu Val Ser Val Gly Ser  
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 75 80 85  
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 Glu Leu Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr  
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Leu Leu Lys Ile Asp Asn Arg Asn Ile Val Glu Tyr Ile Lys Ala Arg
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act cat tta att cgt tgg gtc gga tta tct cgc cag aag tcg aat gag 594
Thr His Leu Ile Arg Trp Val Gly Leu Ser Arg Gln Lys Ser Asn Glu
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gtc tgg aag tgg gag gat ggc tcg gtt atc tca gaa aat atg ttt gag 642
Val Trp Lys Trp Glu Asp Gly Ser Val Ile Ser Glu Asn Met Phe Glu
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Phe Leu Glu Asp Gly Lys Gly Asn Met Asn Cys Ala Tyr Phe His Asn
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Gly Lys Met His Pro Thr Phe Cys Glu Asn Lys His Tyr Leu Met Cys
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Glu Arg Lys Ala Gly Met Thr Lys Val Asp Gln Leu Pro
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Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn Tyr Leu Gln Asp
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Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln Leu Ala Lys Arg Phe
65          70          75          80
Cys Gln Tyr Val Val Lys Gln Ser Glu Leu Lys Gly Thr Phe Lys Gly
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His Lys Cys Ser Pro Cys Asp Thr Asn Trp Arg Tyr Tyr Gly Asp Ser
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Cys Tyr Gly Phe Phe Arg His Asn Leu Thr Trp Glu Glu Ser Lys Gln
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aacacaccaa ggaaaattaa tataggaaaa atttaaaaag ttattagagg actgaaaata 180
taaaaatgga acactgaaag acacagagtt tttattttca gcactgcagc tctg atg 237
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Val Gln Leu His Gln Asp Thr Asp Pro Gln Ile Pro Lys Gly Gln Pro
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Cys Thr Leu Asn Ser Ser Glu Gly Gly Ala Arg Pro Ala Val Pro His
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Ala Asp Ser Gly Pro Pro Pro Lys Asn Asn Met Glu Gly Leu Asn Val
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Ser Lys Glu Asp Glu Glu Gly
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<400> 6
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His Thr Leu Phe Ser Ser Ala Leu Asp Arg Trp Leu His Asn Asp Ser
          35          40          45
Phe Ile Met Ala Val Gly Glu Pro Leu Val His Ile Arg Val Thr Leu
          50          55          60
Leu Leu Leu Trp Phe Gly Met Phe Leu Ser Ile Ser Gly His Ser Gln
65          70          75          80
Ala Arg Pro Ser Gln Tyr Phe Thr Ser Pro Glu Val Val Ile Pro Leu
          85          90          95
Lys Val Ile Ser Arg Gly Arg Gly Ala Lys Ala Pro Gly Trp Leu Ser
          100          105          110
Tyr Ser Leu Arg Phe Gly Gly Gln Arg Tyr Ile Val His Met Arg Val
          115          120          125
Asn Lys Leu Leu Phe Ala Ala His Leu Pro Val Phe Thr Tyr Thr Glu
          130          135          140
Gln His Ala Leu Leu Gln Asp Gln Pro Phe Ile Gln Asp Asp Cys Tyr

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145													150					155					160
Tyr	His	Gly	Tyr	Val	Glu	Gly	Val	Pro	Glu	Ser	Leu	Val	Ala	Leu	Ser								
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Thr	Cys	Ser	Gly	Gly	Phe	Leu	Gly	Met	Leu	Gln	Ile	Asn	Asp	Leu	Val								
				180					185					190									
Tyr	Glu	Ile	Lys	Pro	Ile	Ser	Val	Ser	Ala	Thr	Phe	Glu	His	Leu	Val								
				195					200					205									
Tyr	Lys	Ile	Asp	Ser	Asp	Asp	Thr	Gln	Phe	Pro	Pro	Met	Arg	Cys	Gly								
				210					215					220									
Leu	Thr	Glu	Glu	Lys	Ile	Ala	His	Gln	Met	Glu	Leu	Gln	Leu	Ser	Tyr								
225					230					235					240								
Asn	Phe	Thr	Leu	Lys	Gln	Ser	Ser	Phe	Val	Gly	Trp	Trp	Thr	His	Gln								
				245					250					255									
Arg	Phe	Val	Glu	Leu	Val	Val	Val	Val	Asp	Asn	Ile	Arg	Tyr	Leu	Phe								
				260					265					270									
Ser	Gln	Ser	Asn	Ala	Thr	Thr	Val	Gln	His	Glu	Val	Phe	Asn	Val	Val								
				275					280					285									
Asn	Ile	Val	Asp	Ser	Phe	Tyr	His	Pro	Leu	Glu	Val	Asp	Val	Ile	Leu								
				290					295					300									
Thr	Gly	Ile	Asp	Ile	Trp	Thr	Ala	Ser	Asn	Pro	Leu	Pro	Thr	Ser	Gly								
305					310					315					320								
Asp	Leu	Asp	Asn	Val	Leu	Glu	Asp	Phe	Ser	Ile	Trp	Lys	Asn	Tyr	Asn								
				325					330					335									
Leu	Asn	Asn	Arg	Leu	Gln	His	Asp	Val	Ala	His	Leu	Phe	Ile	Lys	Asp								
				340					345					350									
Thr	Gln	Gly	Met	Lys	Leu	Gly	Val	Ala	Tyr	Val	Lys	Gly	Ile	Cys	Gln								
				355					360					365									
Asn	Pro	Phe	Asn	Thr	Gly	Val	Asp	Val	Phe	Glu	Asp	Asn	Arg	Leu	Val								
				370					375					380									
Val	Phe	Ala	Ile	Thr	Leu	Gly	His	Glu	Leu	Gly	His	Asn	Leu	Gly	Met								
385					390					395					400								
Gln	His	Asp	Thr	Gln	Trp	Cys	Val	Cys	Glu	Leu	Gln	Trp	Cys	Ile	Met								
				405					410					415									
His	Ala	Tyr	Arg	Lys	Val	Thr	Thr	Lys	Phe	Ser	Asn	Cys	Ser	Tyr	Ala								
				420					425					430									
Gln	Tyr	Trp	Asp	Ser	Thr	Ile	Ser	Ser	Gly	Leu	Cys	Ile	Gln	Pro	Pro								
				435					440					445									
Pro	Tyr	Pro	Gly	Asn	Ile	Phe	Arg	Leu	Lys	Tyr	Cys	Gly	Asn	Leu	Val								
				450					455					460									
Val	Glu	Glu	Gly	Glu	Glu	Cys	Asp	Cys	Gly	Thr	Ile	Arg	Gln	Cys	Ala								
465					470					475					480								
Lys	Asp	Pro	Cys	Cys	Leu	Leu	Asn	Cys	Thr	Leu	His	Pro	Gly	Ala	Ala								
				485					490					495									
Cys	Ala	Phe	Gly	Ile	Cys	Cys	Lys	Asp	Cys	Lys	Phe	Leu	Pro	Ser	Gly								
				500					505					510									
Thr	Leu	Cys	Arg	Gln	Gln	Val	Gly	Glu	Cys	Asp	Leu	Pro	Glu	Trp	Cys								



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gctgccctgt tgcagggagg cggtagccct tctgttgcta gaccgagcct gtgggatata 240
ccaaggcaga ggagcccata gcc atg agg agc ctc ggg gcc ctg ctc ttg ctg 293
                               Met Arg Ser Leu Gly Ala Leu Leu Leu Leu
                               -15                               -10

ctg agc gcc tgc ctg gcg gtg agc gct ggc cct gtg cca acg ccg ccc 341
Leu Ser Ala Cys Leu Ala Val Ser Ala Gly Pro Val Pro Thr Pro Pro
                               -5                               1                               5

gac aac atc caa gtg cag gaa aac ttc aat atc tct cgg atc tat ggg 389
Asp Asn Ile Gln Val Gln Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly
                               10                               15                               20

aag tgg tac aac ctg gcc atc ggt tcc acc tgc ccc tgg ctg aag aag 437
Lys Trp Tyr Asn Leu Ala Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys
                               25                               30                               35

atc atg gac agg atg aca gtg agc acg ctg gtg ctg gga gag ggc gct 485
Ile Met Asp Arg Met Thr Val Ser Thr Leu Val Leu Gly Glu Gly Ala
40                               45                               50                               55

aca gag gcg gag atc agc atg acc agc act cgt tgg cgg aaa ggt gtc 533
Thr Glu Ala Glu Ile Ser Met Thr Ser Thr Arg Trp Arg Lys Gly Val
                               60                               65                               70

tgt gag gag acg tct gga gct tat gag aaa aca gat act gat ggg aag 581
Cys Glu Glu Thr Ser Gly Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys
75                               80                               85

ttt ctc tat cac aaa tcc aaa tgg aac ata acc atg gag tcc tat gtg 629
Phe Leu Tyr His Lys Ser Lys Trp Asn Ile Thr Met Glu Ser Tyr Val
90                               95                               100

gtc cac acc aac tat gat gag tat gcc att ttc ctg acc aag aaa ttc 677
Val His Thr Asn Tyr Asp Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe
105                               110                               115

agc cgc cat cat gga ccc acc att act gcc aag ctc tac ggg cgg gcg 725
Ser Arg His His Gly Pro Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala
120                               125                               130                               135

ccg cag ctg agg gaa act ctc ctg cag gac ttc aga gtg gtt gcc cag 773
Pro Gln Leu Arg Glu Thr Leu Leu Gln Asp Phe Arg Val Val Ala Gln
140                               145                               150

ggg gtg ggc atc cct gag gac tcc atc ttc acc atg gct gac cga ggt 821
Gly Val Gly Ile Pro Glu Asp Ser Ile Phe Thr Met Ala Asp Arg Gly
155                               160                               165

gaa tgt gtc cct ggg gag cag gaa cca gag ccc atc tta atc ccg aga 869
Glu Cys Val Pro Gly Glu Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg
170                               175                               180

gtc cgg agg gct gct acc cca aga aga gga agg atc agg ggg tgg gca 917
Val Arg Arg Ala Ala Thr Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala
185                               190                               195

act ggt aac tgaagtcacc aagaaagaag attcctgccca gctgggctac 966
Thr Gly Asn
200

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gccggtctgc aagtcagagg atggccagtg tctgtcccgg ggtcctgtgg caggcagcgc 1386

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1436

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 <213> Homo sapiens

<220>  
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                   1                  5                  10  
 Glu Asn Phe Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala  
           15                  20                  25  
 Ile Gly Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr  
                   35                  40                  45  
 Val Ser Thr Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser  
                   50                  55                  60  
 Met Thr Ser Thr Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly  
                   65                  70                  75  
 Ala Tyr Glu Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser  
                   80                  85                  90  
 Lys Trp Asn Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp  
                   95                  100                  105  
 Glu Tyr Ala Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro  
                   110                  115                  120                  125  
 Thr Ile Thr Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr  
                   130                  135                  140  
 Leu Leu Gln Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu  
                   145                  150                  155  
 Asp Ser Ile Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu  
                   160                  165                  170  
 Gln Glu Pro Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Ala Thr  
                   175                  180                  185  
 Pro Arg Arg Gly Arg Ile Arg Gly Trp Ala Thr Gly Asn  
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 <212> DNA  
 <213> Homo sapiens

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<220>  
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<220>  
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<220>  
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 Met Gln Arg Leu Gln Val Val  
 -35 -30  
 ctg ggc cac ctg agg ggt ccg gcc gat tcc ggc tgg atg ccg cag gcc 161  
 Leu Gly His Leu Arg Gly Pro Ala Asp Ser Gly Trp Met Pro Gln Ala  
 -25 -20 -15  
 gcg cct tgc ctg agc ggt gcc ccg cag gcc tcg gcc gcg gac gtg gtg 209  
 Ala Pro Cys Leu Ser Gly Ala Pro Gln Ala Ser Ala Ala Asp Val Val  
 -10 -5 1  
 gtg gtg cac ggg cgg cgc acg gcc atc tgc cgg gcg ggc cgc ggc ggc 257  
 Val Val His Gly Arg Arg Thr Ala Ile Cys Arg Ala Gly Arg Gly Gly  
 5 10 15 20  
 ttc aag gac acc acc ccc gac gag ctt ctc tcg gca gtc atg acc gcg 305  
 Phe Lys Asp Thr Thr Pro Asp Glu Leu Leu Ser Ala Val Met Thr Ala  
 25 30 35  
 gtt ctc aag gac gtg aat ctg agg ccg gaa cag ctg ggg gac atc tgt 353  
 Val Leu Lys Asp Val Asn Leu Arg Pro Glu Gln Leu Gly Asp Ile Cys  
 40 45 50  
 gtc gga aat gtg ctg cag cct ggg gcc ggg gca atc atg gcc cga atc 401  
 Val Gly Asn Val Leu Gln Pro Gly Ala Gly Ala Ile Met Ala Arg Ile  
 55 60 65  
 gcc cag ttt ctg agt gac atc ccg gag act gtg cct ttg tcc act gtc 449  
 Ala Gln Phe Leu Ser Asp Ile Pro Glu Thr Val Pro Leu Ser Thr Val  
 70 75 80  
 aat aga cag tgt tcg tcg ggg cta cag gca gtg gcc agc ata gca ggg 497  
 Asn Arg Gln Cys Ser Ser Gly Leu Gln Ala Val Ala Ser Ile Ala Gly  
 85 90 95 100  
 tgg agt cca tgt ccc tgg ctg aca gag gga acc ctg gaa ata tta ctt 545  
 Trp Ser Pro Cys Pro Trp Leu Thr Glu Gly Thr Leu Glu Ile Leu Leu  
 105 110 115  
 cgc gct tgatggagaa ggagaaggcc agagattgcc tgattcctat ggggataacc 601  
 Arg Ala  
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 gcttcccagc agaaggcagc aagagcccag agcaagggct gtttccaagc tgagattgtg 721  
 cctgtgacca ccacggtcca tgatgacaag ggcaccaaga ggagcatcac tgtgaccag 781  
 gatgagggta tccgccccag caccaccatg gagggcctgg ccaaactgaa gcctgccttc 841  
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 <213> Homo sapiens

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			-15						-10					-5	
Ala	Ser	Ala	Ala	Asp	Val	Val	Val	Val	His	Gly	Arg	Arg	Thr	Ala	Ile
			1					5				10			
Cys	Arg	Ala	Gly	Arg	Gly	Gly	Phe	Lys	Asp	Thr	Thr	Pro	Asp	Glu	Leu
15						20					25				
Leu	Ser	Ala	Val	Met	Thr	Ala	Val	Leu	Lys	Asp	Val	Asn	Leu	Arg	Pro
30					35					40					45
Glu	Gln	Leu	Gly	Asp	Ile	Cys	Val	Gly	Asn	Val	Leu	Gln	Pro	Gly	Ala
			50						55					60	
Gly	Ala	Ile	Met	Ala	Arg	Ile	Ala	Gln	Phe	Leu	Ser	Asp	Ile	Pro	Glu
			65					70					75		
Thr	Val	Pro	Leu	Ser	Thr	Val	Asn	Arg	Gln	Cys	Ser	Ser	Gly	Leu	Gln
		80					85					90			
Ala	Val	Ala	Ser	Ile	Ala	Gly	Trp	Ser	Pro	Cys	Pro	Trp	Leu	Thr	Glu
	95					100					105				
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 <212> DNA  
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<220>  
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 <222> 2251..2266

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 atcatgaaag gtgaaatcat tacggaattg cttaaataata taatttgaat ctggatttaa 180  
 aaataataaaa tgtgatcagg atg ccc ttc tct cat ctg tct acc tac agc ctg 233  
 Met Pro Phe Ser His Leu Ser Thr Tyr Ser Leu  
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 Val Trp Val Met Ala Ala Val Val Leu Cys Thr Ala Gln Val Gln Val  
 -10 -5 1  
 gtg acc cag gat gaa aga gag cag ctg tac aca act gct tcc tta aaa 329  
 Val Thr Gln Asp Glu Arg Glu Gln Leu Tyr Thr Thr Ala Ser Leu Lys  
 5 10 15 20  
 tgc tct ctg caa aat gcc cag gaa gcc ctc att gtg aca tgg cag aaa 377  
 Cys Ser Leu Gln Asn Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys  
 25 30 35  
 aag aaa gct gta agc cca gaa aac atg gtc acc ttc agc gag aac cat 425  
 Lys Lys Ala Val Ser Pro Glu Asn Met Val Thr Phe Ser Glu Asn His  
 40 45 50  
 ggg gtg gtg atc cag cct gcc tat aag gac aag ata aac att acc cag 473  
 Gly Val Val Ile Gln Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln  
 55 60 65  
 ctg gga ctc caa aac tca acc atc acc ttc tgg aat atc acc ctg gag 521  
 Leu Gly Leu Gln Asn Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu  
 70 75 80  
 gat gaa ggg tgt tac atg tgt ctc ttc aat acc ttt ggt ttt ggg aag 569  
 Asp Glu Gly Cys Tyr Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys  
 85 90 95 100  
 atc tca gga acg gcc tgc ctc acc gtc tat gta cag ccc ata gta tcc 617  
 Ile Ser Gly Thr Ala Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser  
 105 110 115  
 ctt cac tac aaa ttc tct gaa gac cac cta aat atc act tgc tct gcc 665  
 Leu His Tyr Lys Phe Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala

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act gcc cgc cca gcc ccc atg gtc ttc tgg aag gtc cct cgg tca ggg 713
Thr Ala Arg Pro Ala Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly
      135      140      145
att gaa aat agt aca gtg act ctg tct cac cca aat ggg acc acg tct 761
Ile Glu Asn Ser Thr Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser
      150      155      160
gtt acc agc atc ctc cat atc aaa gac cct aag aat cag gtg ggg aag 809
Val Thr Ser Ile Leu His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys
      165      170      175      180
gag gtg atc tgc cag gtg ctg cac ctg ggg act gtg acc gac ttt aag 857
Glu Val Ile Cys Gln Val Leu His Leu Gly Thr Val Thr Asp Phe Lys
      185      190      195
caa acc gtc aac aaa ggc tat tgg ttt tca gtt ccg cta ttg cta agc 905
Gln Thr Val Asn Lys Gly Tyr Trp Phe Ser Val Pro Leu Leu Leu Ser
      200      205      210
att gtt tcc ctg gta att ctt ctc gtc cta atc tca atc tta ctg tac 953
Ile Val Ser Leu Val Ile Leu Val Leu Ile Ser Ile Leu Leu Tyr
      215      220      225
tgg aaa cgt cac cgg aat cag gac cga gag ccc taaataagtc acacagcacc 1006
Trp Lys Arg His Arg Asn Gln Asp Arg Glu Pro
      230      235
ctgaaagtga ttccctggtc tacttgaatt tgacacaaga gaaaagcagg agaaaaaggg 1066
gccattctcc aaaggacctg aaagagcaaa agaggtggga gcgaaagcct taaggatccc 1126
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gtggaatgat gttgaatctt taataaccat aattagttgc tttttcagta tcttctgctt 2086
tgtctgtgtc tatccagtgg cctaggaatt aaagtgtgta ttgttttcgc tgttaaattg 2146
gatatttata tatatatata tagcaagatt ttcattgtgt atttaattct gtattgtttc 2206
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<210> 12  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

<400> 12



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      -5                      1                      5
Arg Glu Gln Leu Tyr Thr Thr Ala Ser Leu Lys Cys Ser Leu Gln Asn
10                      15                      20                      25
Ala Gln Glu Ala Leu Ile Val Thr Trp Gln Lys Lys Lys Ala Val Ser
      30                      35                      40
Pro Glu Asn Met Val Thr Phe Ser Glu Asn His Gly Val Val Ile Gln
      45                      50                      55
Pro Ala Tyr Lys Asp Lys Ile Asn Ile Thr Gln Leu Gly Leu Gln Asn
      60                      65                      70
Ser Thr Ile Thr Phe Trp Asn Ile Thr Leu Glu Asp Glu Gly Cys Tyr
      75                      80                      85
Met Cys Leu Phe Asn Thr Phe Gly Phe Gly Lys Ile Ser Gly Thr Ala
90                      95                      100                      105
Cys Leu Thr Val Tyr Val Gln Pro Ile Val Ser Leu His Tyr Lys Phe
      110                      115                      120
Ser Glu Asp His Leu Asn Ile Thr Cys Ser Ala Thr Ala Arg Pro Ala
      125                      130                      135
Pro Met Val Phe Trp Lys Val Pro Arg Ser Gly Ile Glu Asn Ser Thr
      140                      145                      150
Val Thr Leu Ser His Pro Asn Gly Thr Thr Ser Val Thr Ser Ile Leu
      155                      160                      165
His Ile Lys Asp Pro Lys Asn Gln Val Gly Lys Glu Val Ile Cys Gln
170                      175                      180                      185
Val Leu His Leu Gly Thr Val Thr Asp Phe Lys Gln Thr Val Asn Lys
      190                      195                      200
Gly Tyr Trp Phe Ser Val Pro Leu Leu Leu Ser Ile Val Ser Leu Val
      205                      210                      215
Ile Leu Leu Val Leu Ile Ser Ile Leu Leu Tyr Trp Lys Arg His Arg
      220                      225                      230
Asn Gln Asp Arg Glu Pro
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<213> Homo sapiens

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<221> polyA\_site

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tgaga atg gag aga atg tta cct ctc ctg act ctg ggg ctc ttg gcg gct 110
      Met Glu Arg Met Leu Pro Leu Leu Thr Leu Gly Leu Leu Ala Ala
            -20                    -15                    -10
ggg ttc tgc cct gct gtc ctc tgc cac cct aac agc cca ctt gac gag 158
Gly Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu
            -5                    1                    5
gag aat ctg acc cag gag aac caa gac cga ggg aca cac gtg gac ctc 206
Glu Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu
            10                    15                    20
gga tta gcc tcc gcc aac gtg gac ttc gct ctc agc ctg tac aag cag 254
Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Leu Ser Leu Tyr Lys Gln
            25                    30                    35                    40
tta gtc ctg aag gcc cct gat aag aat gtc atc ttc tcc cca ctg agc 302
Leu Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser
            45                    50                    55
atc tcc acc gcc ttg gcc ttc ctg tct ctg ggg gcc cat aat acc acc 350
Ile Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr
            60                    65                    70
ctg aca gag att ctc aaa ggc ctc aag ttc aac ctc acg gag act tct 398
Leu Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser
            75                    80                    85
gag gca gaa att cac cag agc ttc cag cac ctc ctg cgc acc ctc aat 446
Glu Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn
            90                    95                    100
cag tcc agc gat gag ctg cag ctg agt atg gga aat gcc atg ttt gtc 494
Gln Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val
            105                    110                    115                    120
aaa gag caa ctc agt ctg ctg gac agg ttc acg gag gat gcc aag agg 542
Lys Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg
            125                    130                    135
ctg tat ggc tcc gag gcc ttt gcc act gac ttt cag gac tca gct gca 590
Leu Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala
            140                    145                    150
gct aag aag ctc atc aac gac tac gtg aag aat gga act agg ggg aaa 638
Ala Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys
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atc aca gat ctg atc aag gac ctt gac tcg cag aca atg atg gtc ctg 686
Ile Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu
            170                    175                    180
gtg aat tac atc ttc ttt aaa gcc aaa tgg gag atg ccc ttt gac ccc 734
Val Asn Tyr Ile Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro
            185                    190                    195                    200
caa gat act cat cag tca agg ttc tac ttg agc aag aaa aag tgg gta 782
Gln Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val
            205                    210                    215
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0976410 "101501"

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gac	gag	gag	ctg	tcc	tgc	acc	gtg	gtg	gag	ctg	aag	tac	aca	ggc	aat	878
Asp	Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	Tyr	Thr	Gly	Asn	
		235					240					245				
gcc	agc	gca	ctc	ttc	atc	ctc	cct	gat	caa	gac	aag	atg	gag	gaa	gtg	926
Ala	Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	Met	Glu	Glu	Val	
		250				255					260					
gaa	gcc	atg	ctg	ctc	cca	gag	acc	ctg	aag	cgg	tgg	aga	gac	tct	ctg	974
Glu	Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	Arg	Asp	Ser	Leu	
265					270					275					280	
gag	ttc	aga	gag	ata	ggt	gag	ctc	tac	ctg	cca	aag	ttt	tcc	atc	tcg	1022
Glu	Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Ser	
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agg	gac	tat	aac	ctg	aac	gac	ata	ctt	ctc	cag	ctg	ggc	att	gag	gaa	1070
Arg	Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Leu	Gln	Leu	Gly	Ile	Glu	Glu	
			300					305					310			
gcc	ttc	acc	agc	aag	gct	gac	ctg	tca	ggg	atc	aca	ggg	gcc	agg	aac	1118
Ala	Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	Gly	Ala	Arg	Asn	
		315					320					325				
cta	gca	gtc	tcc	cag	gtg	gtc	cat	aag	gct	gtg	ctt	gat	gta	ttt	gag	1166
Leu	Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	Asp	Val	Phe	Glu	
		330				335					340					
gag	ggc	aca	gaa	gca	tct	gct	gcc	aca	gca	gtc	aaa	atc	acc	ctc	ctt	1214
Glu	Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	Ile	Thr	Leu	Leu	
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tct	gca	tta	gtg	gag	aca	agg	acc	att	gtg	cgt	ttc	aac	agg	ccc	ttc	1262
Ser	Ala	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	Asn	Arg	Pro	Phe	
				365				370						375		
ctg	atg	atc	att	gtc	cct	aca	gac	acc	cag	aac	atc	ttc	ttc	atg	agc	1310
Leu	Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile	Phe	Phe	Met	Ser	
			380					385					390			
aaa	gtc	acc	aat	ccc	aag	caa	gcc	tagagcttg	c	catcaagcag	tggggctctc					1364
Lys	Val	Thr	Asn	Pro	Lys	Gln	Ala									
		395					400									
agtaa	ggaac		ttggaatg	ca	agctgg	gatgc		ctgggtctct		gggcacagcc		tggccccctgt				1424
gcacc	gagtg		gccatgg	cat	gtgtgg	ccct		gtctgcttat		ccttggaagg		tgacagcgat				1484
tccct	gtgta		gctctcac	at	gcacagg	gggc		ccatggactc		ttcagtctgg		aggggtcctgg				1544
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Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
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Val	Leu	Lys	Ala	Pro	Asp	Lys	Asn	Val	Ile	Phe	Ser	Pro	Leu	Ser	Ile
			45					50					55		
Ser	Thr	Ala	Leu	Ala	Phe	Leu	Ser	Leu	Gly	Ala	His	Asn	Thr	Thr	Leu
		60					65					70			
Thr	Glu	Ile	Leu	Lys	Gly	Leu	Lys	Phe	Asn	Leu	Thr	Glu	Thr	Ser	Glu
	75					80					85				
Ala	Glu	Ile	His	Gln	Ser	Phe	Gln	His	Leu	Leu	Arg	Thr	Leu	Asn	Gln
90					95					100					105
Ser	Ser	Asp	Glu	Leu	Gln	Leu	Ser	Met	Gly	Asn	Ala	Met	Phe	Val	Lys
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Glu	Gln	Leu	Ser	Leu	Leu	Asp	Arg	Phe	Thr	Glu	Asp	Ala	Lys	Arg	Leu
			125					130					135		
Tyr	Gly	Ser	Glu	Ala	Phe	Ala	Thr	Asp	Phe	Gln	Asp	Ser	Ala	Ala	Ala
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Lys	Lys	Leu	Ile	Asn	Asp	Tyr	Val	Lys	Asn	Gly	Thr	Arg	Gly	Lys	Ile
	155					160					165				
Thr	Asp	Leu	Ile	Lys	Asp	Leu	Asp	Ser	Gln	Thr	Met	Met	Val	Leu	Val
170					175					180					185
Asn	Tyr	Ile	Phe	Phe	Lys	Ala	Lys	Trp	Glu	Met	Pro	Phe	Asp	Pro	Gln
				190					195					200	
Asp	Thr	His	Gln	Ser	Arg	Phe	Tyr	Leu	Ser	Lys	Lys	Lys	Trp	Val	Met
		205						210					215		
Val	Pro	Met	Met	Ser	Leu	His	His	Leu	Thr	Ile	Pro	Tyr	Phe	Arg	Asp
		220					225					230			
Glu	Glu	Leu	Ser	Cys	Thr	Val	Val	Glu	Leu	Lys	Tyr	Thr	Gly	Asn	Ala
	235					240					245				
Ser	Ala	Leu	Phe	Ile	Leu	Pro	Asp	Gln	Asp	Lys	Met	Glu	Glu	Val	Glu
250					255					260					265
Ala	Met	Leu	Leu	Pro	Glu	Thr	Leu	Lys	Arg	Trp	Arg	Asp	Ser	Leu	Glu
				270					275					280	
Phe	Arg	Glu	Ile	Gly	Glu	Leu	Tyr	Leu	Pro	Lys	Phe	Ser	Ile	Ser	Arg
		285						290					295		
Asp	Tyr	Asn	Leu	Asn	Asp	Ile	Leu	Leu	Gln	Leu	Gly	Ile	Glu	Glu	Ala
		300					305					310			
Phe	Thr	Ser	Lys	Ala	Asp	Leu	Ser	Gly	Ile	Thr	Gly	Ala	Arg	Asn	Leu
	315					320					325				
Ala	Val	Ser	Gln	Val	Val	His	Lys	Ala	Val	Leu	Asp	Val	Phe	Glu	Glu
330					335					340					345
Gly	Thr	Glu	Ala	Ser	Ala	Ala	Thr	Ala	Val	Lys	Ile	Thr	Leu	Leu	Ser
				350					355					360	
Ala	Leu	Val	Glu	Thr	Arg	Thr	Ile	Val	Arg	Phe	Asn	Arg	Pro	Phe	Leu
		365						370				375			
Met	Ile	Ile	Val	Pro	Thr	Asp	Thr	Gln	Asn	Ile	Phe	Phe	Met	Ser	Lys
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Val	Thr	Asn	Pro	Lys	Gln	Ala									
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cgggccttcg ggtgcgcgtc tcgcctctag cc atg ggg tcc gca gcg ttg gag 173
                                Met Gly Ser Ala Ala Leu Glu
                                1 5
atc ctg ggc ctg gtg ctg tgc ctg gtg ggc tgg ggg ggt ctg atc ctg 221
Ile Leu Gly Leu Val Leu Cys Leu Val Gly Trp Gly Gly Leu Ile Leu
10 15 20
gcg tgc ggg ctg ccc atg tgg cag gtg acc gcc ttc ctg gac cac aac 269
Ala Cys Gly Leu Pro Met Trp Gln Val Thr Ala Phe Leu Asp His Asn
25 30 35
atc gtg acg gcg cag acc acc tgg aag ggg ctg tgg atg tcg tgc gtg 317
Ile Val Thr Ala Gln Thr Thr Trp Lys Gly Leu Trp Met Ser Cys Val
40 45 50 55
gtg cag agc acc ggg cac atg cag tgc aaa gtg tac gac tcg gtg ctg 365
Val Gln Ser Thr Gly His Met Gln Cys Lys Val Tyr Asp Ser Val Leu
60 65 70
gct ctg agc acc gag gtg cag gcg gcg cgg gcg ctc acc gtg agc gcc 413
Ala Leu Ser Thr Glu Val Gln Ala Ala Arg Ala Leu Thr Val Ser Ala
75 80 85
gtg ctg ctg gcg ttc gtt gcg ctc ttc gtg acc ctg gcg ggc gcg cag 461
Val Leu Leu Ala Phe Val Ala Leu Phe Val Thr Leu Ala Gly Ala Gln
90 95 100
tgc acc acc tgc gtg gcc ccg ggc ccg gcc aag gcg cgt gtg gcc ctc 509
Cys Thr Thr Cys Val Ala Pro Gly Pro Ala Lys Ala Arg Val Ala Leu
105 110 115
acg gga ggc gtg ctc tac ctg ttt tgc ggg ctg ctg gcg ctc gtg cca 557
Thr Gly Gly Val Leu Tyr Leu Phe Cys Gly Leu Leu Ala Leu Val Pro
120 125 130 135
ctc tgc tgg ttc gcc aac att gtc gtc cgc gag ttt tac gac ccg tct 605
Leu Cys Trp Phe Ala Asn Ile Val Val Arg Glu Phe Tyr Asp Pro Ser

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Val	Pro	Val	Ser	Gln	Lys	Tyr	Glu	Leu	Gly	Ala	Ala	Leu	Tyr	Ile	Gly						
										155			160			165					
tgg	gcg	gcc	acc	gcg	ctg	ctc	atg	gta	ggc	ggc	tgc	ctc	ttg	tgc	tgc		701				
Trp	Ala	Ala	Thr	Ala	Leu	Leu	Met	Val	Gly	Gly	Cys	Leu	Leu	Cys	Cys						
										170			175			180					
ggc	gcc	tgg	gtc	tgc	acc	ggc	cgt	ccc	gac	ctc	agc	ttc	ccc	gtg	aag		749				
Gly	Ala	Trp	Val	Cys	Thr	Gly	Arg	Pro	Asp	Leu	Ser	Phe	Pro	Val	Lys						
										185			190			195					
tac	tca	gcg	ccg	cgg	cgg	ccc	acg	gcc	acc	ggc	gac	aac	gac	aag	aag		797				
Tyr	Ser	Ala	Pro	Arg	Arg	Pro	Thr	Ala	Thr	Gly	Asp	Asn	Asp	Lys	Lys						
200										205			210			215					
aac	tac	gtc	tgagggcgct	gggcacggcc	gggccccctcc	tgccagccac											846				
Asn	Tyr	Val																			
gcctgcgagg	cgcttgataa	gcctggggag	ccccgcgatgg	accgcgggctt	ccgcgcgggta	906															
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<213> Homo sapiens
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			20					25					30			
Thr	Ala	Phe	Leu	Asp	His	Asn	Ile	Val	Thr	Ala	Gln	Thr	Thr	Trp	Lys	
		35					40					45				
Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly	His	Met	Gln	Cys	
	50					55					60					
Lys	Val	Tyr	Asp	Ser	Val	Leu	Ala	Leu	Ser	Thr	Glu	Val	Gln	Ala	Ala	
65					70					75					80	
Arg	Ala	Leu	Thr	Val	Ser	Ala	Val	Leu	Leu	Ala	Phe	Val	Ala	Leu	Phe	
				85					90					95		
Val	Thr	Leu	Ala	Gly	Ala	Gln	Cys	Thr	Thr	Cys	Val	Ala	Pro	Gly	Pro	
			100					105					110			
Ala	Lys	Ala	Arg	Val	Ala	Leu	Thr	Gly	Gly	Val	Leu	Tyr	Leu	Phe	Cys	
		115					120					125				
Gly	Leu	Leu	Ala	Leu	Val	Pro	Leu	Cys	Trp	Phe	Ala	Asn	Ile	Val	Val	
	130					135					140					
Arg	Glu	Phe	Tyr	Asp	Pro	Ser	Val	Pro	Val	Ser	Gln	Lys	Tyr	Glu	Leu	
145					150					155					160	
Gly	Ala	Ala	Leu	Tyr	Ile	Gly	Trp	Ala	Ala	Thr	Ala	Leu	Leu	Met	Val	
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 Thr Gly Asp Asn Asp Lys Lys Asn Tyr Val  
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 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly  
 1 5 10 15  
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155  
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys  
 20 25 30  
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203  
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu  
 35 40 45  
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251  
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu  
 50 55 60  
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299  
 Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro  
 65 70 75  
 ctt ggc ctc tat gct gat cag ctc acc atc agc tgg act gtc ctg gtt 347  
 Leu Gly Leu Tyr Ala Asp Gln Leu Thr Ile Ser Trp Thr Val Leu Val  
 80 85 90 95  
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395  
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu

100								105					110					
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Leu	Leu	Tyr	Gly	Leu	Val	Val	Ser	Thr	Ala	Leu	Ile	Trp	His	Pro	Ile			
115								120					125					
aac	aaa	ctg	gct	gcc	ctg	tta	ctg	ctg	ccc	tac	cta	gcc	tgg	ctc	acc	491		
Asn	Lys	Leu	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Tyr	Leu	Ala	Trp	Leu	Thr			
130								135					140					
gtg	act	tca	gcc	ctc	acc	tac	cac	ctg	tgg	agg	gac	agc	ctt	tgt	cca	539		
Val	Thr	Ser	Ala	Leu	Thr	Tyr	His	Leu	Trp	Arg	Asp	Ser	Leu	Cys	Pro			
145								150					155					
gtg	cac	cag	cct	cag	ccc	acg	gag	aag	agt	gac	tgaggcccta				gggcatggga		592	
Val	His	Gln	Pro	Gln	Pro	Thr	Glu	Lys	Ser	Asp								
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acccccaatg			ggaccaccct			cctgggtccc			ctgggtccgt			ttttccttag			aaatcagaga			712
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aaaaaaaaaa																782		

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Ile	Leu	Val	Trp	Leu	Phe	Thr	Arg	Asp	His	Met	Ser	Gly	Trp	Cys	Glu	
			20					25					30			
Gly	Pro	Arg	Met	Leu	Ser	Trp	Cys	Pro	Phe	Tyr	Lys	Val	Leu	Leu	Leu	
			35				40					45				
Val	Gln	Thr	Ala	Ile	Tyr	Ser	Val	Val	Gly	Tyr	Ala	Ser	Tyr	Leu	Val	
	50					55					60					
Trp	Lys	Asp	Leu	Gly	Gly	Gly	Leu	Gly	Trp	Pro	Leu	Ala	Leu	Pro	Leu	
65					70					75					80	
Gly	Leu	Tyr	Ala	Asp	Gln	Leu	Thr	Ile	Ser	Trp	Thr	Val	Leu	Val	Leu	
				85					90					95		
Phe	Phe	Thr	Val	His	Asn	Pro	Gly	Leu	Ala	Leu	Leu	His	Leu	Leu	Leu	
			100					105					110			
Leu	Tyr	Gly	Leu	Val	Val	Ser	Thr	Ala	Leu	Ile	Trp	His	Pro	Ile	Asn	
		115					120					125				
Lys	Leu	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Tyr	Leu	Ala	Trp	Leu	Thr	Val	
	130					135					140					
Thr	Ser	Ala	Leu	Thr	Tyr	His	Leu	Trp	Arg	Asp	Ser	Leu	Cys	Pro	Val	
145					150					155					160	
His	Gln	Pro	Gln	Pro	Thr	Glu	Lys	Ser	Asp							
				165					170							

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<210> 19
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<212> DNA
<213> Homo sapiens
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<222> 1..62

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<221> CDS

<222> 63..572

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<222> 573..789

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<221> polyA\_signal

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<222> 774..789

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ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
1 5 10 15
ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt ttg tgt 155
Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys
20 25 30
gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
35 40 45
ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
50 55 60
gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
Val Trp Lys Asp Leu Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
65 70 75
ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
80 85 90 95
ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
100 105 110
ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
115 120 125
aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
130 135 140
gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
145 150 155
gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
160 165 170
gaggagggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652

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cacccaatg ggaccacct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
aatgggaaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactct 772
caaaaaaaaa aaaaaaa 789
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1      5      10      15
Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Leu Cys Glu
20     25     30
Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
35     40     45
Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
50     55     60
Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
65     70     75     80
Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
85     90     95
Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
100    105    110
Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
115    120    125
Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
130    135    140
Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
145    150    155    160
His Gln Pro Gln Pro Thr Glu Lys Ser Asp
165    170
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<222> 504..509
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 cgcgtcgggt ggggcgggaa taaagttttt ccaaccaggt ttggggagag ggctggatgg 180  
 gaaggaccct ccctgctgca gacttcatgg caggctgcac tgtgtcccct cggctccacg 240  
 gctgccccgg gggcgctgct ttcgggtttt ctttctagaa tctctggtct gctgctgtgc 300  
 agatggacct gccggcactg ctgtcagaag tgctacgagt ccagctgttg ccagtcaagt 360  
 gaggatgaag ttgaaattct gggacctttc cctgctcaga cccctccctg gctg atg 417  
 Met  
 1  
 gcc agc cgg agc agt gac aag gat ggt gac tct gtc cac acg gcc agc 465  
 Ala Ser Arg Ser Ser Asp Lys Asp Gly Asp Ser Val His Thr Ala Ser  
 5 10 15  
 gaa gtc ccg ctg acc cca cgg acc aat tcc ccg gat gga aga cgc tcg 513  
 Glu Val Pro Leu Thr Pro Arg Thr Asn Ser Pro Asp Gly Arg Arg Ser  
 20 25 30  
 tcc tca gac aca tcc aag tct aca tac agc ctg acg cgg agg att tcg 561  
 Ser Ser Asp Thr Ser Lys Ser Thr Tyr Ser Leu Thr Arg Arg Ile Ser  
 35 40 45  
 agt ctt gag tca aga cgt ccc agc tct cca ctc atc gat att aaa ccc 609  
 Ser Leu Glu Ser Arg Arg Pro Ser Ser Pro Leu Ile Asp Ile Lys Pro  
 50 55 60 65  
 atc gag ttt ggc gtt ctc agc gcc aag aag gag ccc atc caa cct tcg 657  
 Ile Glu Phe Gly Val Leu Ser Ala Lys Lys Glu Pro Ile Gln Pro Ser  
 70 75 80  
 gtg ctc aga cgg acc tat aac ccc gac gac tat ttc agg aag ttc gaa 705  
 Val Leu Arg Arg Thr Tyr Asn Pro Asp Asp Tyr Phe Arg Lys Phe Glu  
 85 90 95  
 ccc cac ctg tac tcc ctc gac tcc aac agc gac gat gtg gac tct ctg 753  
 Pro His Leu Tyr Ser Leu Asp Ser Asn Ser Asp Asp Val Asp Ser Leu  
 100 105 110  
 aca gac gag gag atc ctg tcc aag tac cag ctg ggc atg cag cac ttc 801  
 Thr Asp Glu Glu Ile Leu Ser Lys Tyr Gln Leu Gly Met Gln His Phe  
 115 120 125

agc	act	cag	tac	gac	ctg	ctg	cac	aac	cac	ctc	acc	gtg	cgc	gtg	atc	849
Ser	Thr	Gln	Tyr	Asp	Leu	Leu	His	Asn	His	Leu	Thr	Val	Arg	Val	Ile	
130					135					140					145	
gag	gcc	agg	gac	ctg	cca	cct	ccc	atc	tcc	cac	gat	ggc	tcg	cgc	cag	897
Glu	Ala	Arg	Asp	Leu	Pro	Pro	Pro	Ile	Ser	His	Asp	Gly	Ser	Arg	Gln	
				150					155					160		
gac	atg	gcg	cac	tcc	aac	ccc	tac	gtc	aag	atc	tgt	ctc	ctg	cca	gac	945
Asp	Met	Ala	His	Ser	Asn	Pro	Tyr	Val	Lys	Ile	Cys	Leu	Leu	Pro	Asp	
			165					170					175			
cag	aag	aac	tca	aag	cag	acc	ggg	gtc	aaa	cgc	aag	acc	cag	aag	ccc	993
Gln	Lys	Asn	Ser	Lys	Gln	Thr	Gly	Val	Lys	Arg	Lys	Thr	Gln	Lys	Pro	
		180					185					190				
gtg	ttt	gag	gag	cgc	tac	acc	ttc	gag	atc	ccc	ttc	ctg	gag	gcc	cag	1041
Val	Phe	Glu	Glu	Arg	Tyr	Thr	Phe	Glu	Ile	Pro	Phe	Leu	Glu	Ala	Gln	
	195					200					205					
agg	agg	acc	ctg	ctc	ctg	acc	gtg	gtg	gat	ttt	gat	aag	ttc	tcc	cgc	1089
Arg	Arg	Thr	Leu	Leu	Leu	Thr	Val	Val	Asp	Phe	Asp	Lys	Phe	Ser	Arg	
210					215					220					225	
cac	tgt	gtc	att	ggg	aaa	gtt	tct	gtg	cct	ttg	tgt	gaa	gtt	gac	ctg	1137
His	Cys	Val	Ile	Gly	Lys	Val	Ser	Val	Pro	Leu	Cys	Glu	Val	Asp	Leu	
				230					235					240		
gtc	aag	ggc	ggg	cac	tgg	tgg	aag	gcg	ctg	att	ccc	agt	tct	cag	aat	1185
Val	Lys	Gly	Gly	His	Trp	Trp	Lys	Ala	Leu	Ile	Pro	Ser	Ser	Gln	Asn	
			245					250					255			
gaa	gtg	gag	ctg	ggg	gag	ctg	ctt	ctg	tca	ctg	aat	tat	ctc	cca	agt	1233
Glu	Val	Glu	Leu	Gly	Glu	Leu	Leu	Leu	Ser	Leu	Asn	Tyr	Leu	Pro	Ser	
		260					265					270				
gct	ggc	aga	ctg	aat	gtt	gat	gtc	att	cga	gcc	aag	caa	ctt	ctt	cag	1281
Ala	Gly	Arg	Leu	Asn	Val	Asp	Val	Ile	Arg	Ala	Lys	Gln	Leu	Leu	Gln	
	275					280					285					
aca	gat	gtg	agc	caa	ggt	tca	gac	ccc	ttt	gtg	aaa	atc	cag	ctg	gtg	1329
Thr	Asp	Val	Ser	Gln	Gly	Ser	Asp	Pro	Phe	Val	Lys	Ile	Gln	Leu	Val	
290					295					300					305	
cat	gga	ctc	aaa	ctt	gtg	aaa	acc	aag	aag	acg	tcc	ttc	tta	agg	ggc	1377
His	Gly	Leu	Lys	Leu	Val	Lys	Thr	Lys	Lys	Thr	Ser	Phe	Leu	Arg	Gly	
			310						315					320		
aca	att	gat	cct	ttc	tac	aat	gaa	tcc	ttc	agc	ttc	aaa	gtt	ccc	caa	1425
Thr	Ile	Asp	Pro	Phe	Tyr	Asn	Glu	Ser	Phe	Ser	Phe	Lys	Val	Pro	Gln	
			325					330					335			
gaa	gaa	ctg	gaa	aat	gcc	agc	cta	gtg	ttt	aca	gtt	ttc	ggc	cac	aac	1473
Glu	Glu	Leu														

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aaa                                                1726

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Ser	Glu	Val	Pro	Leu	Thr	Pro	Arg	Thr	Asn	Ser	Pro	Asp	Gly	Arg	Arg	
			20					25					30			
Ser	Ser	Ser	Asp	Thr	Ser	Lys	Ser	Thr	Tyr	Ser	Leu	Thr	Arg	Arg	Ile	
			35				40					45				
Ser	Ser	Leu	Glu	Ser	Arg	Arg	Pro	Ser	Ser	Pro	Leu	Ile	Asp	Ile	Lys	
			50			55					60					
Pro	Ile	Glu	Phe	Gly	Val	Leu	Ser	Ala	Lys	Lys	Glu	Pro	Ile	Gln	Pro	
65				70						75					80	
Ser	Val	Leu	Arg	Arg	Thr	Tyr	Asn	Pro	Asp	Asp	Tyr	Phe	Arg	Lys	Phe	
				85					90					95		
Glu	Pro	His	Leu	Tyr	Ser	Leu	Asp	Ser	Asn	Ser	Asp	Asp	Val	Asp	Ser	
			100					105					110			
Leu	Thr	Asp	Glu	Glu	Ile	Leu	Ser	Lys	Tyr	Gln	Leu	Gly	Met	Gln	His	
			115				120					125				
Phe	Ser	Thr	Gln	Tyr	Asp	Leu	Leu	His	Asn	His	Leu	Thr	Val	Arg	Val	
			130			135					140					
Ile	Glu	Ala	Arg	Asp	Leu	Pro	Pro	Pro	Ile	Ser	His	Asp	Gly	Ser	Arg	
145				150						155					160	
Gln	Asp	Met	Ala	His	Ser	Asn	Pro	Tyr	Val	Lys	Ile	Cys	Leu	Leu	Pro	
				165					170					175		
Asp	Gln	Lys	Asn	Ser	Lys	Gln	Thr	Gly	Val	Lys	Arg	Lys	Thr	Gln	Lys	
			180					185					190			
Pro	Val	Phe	Glu	Glu	Arg	Tyr	Thr	Phe	Glu	Ile	Pro	Phe	Leu	Glu	Ala	
			195				200					205				
Gln	Arg	Arg	Thr	Leu	Leu	Leu	Thr	Val	Val	Asp	Phe	Asp	Lys	Phe	Ser	
						215					220					
Arg	His	Cys	Val	Ile	Gly	Lys	Val	Ser	Val	Pro	Leu	Cys	Glu	Val	Asp	
225				230						235					240	
Leu	Val	Lys	Gly	Gly	His	Trp	Trp	Lys	Ala	Leu	Ile	Pro	Ser	Ser	Gln	
			245						250					255		
Asn	Glu	Val	Glu	Leu	Gly	Glu	Leu	Leu	Leu	Ser	Leu	Asn	Tyr	Leu	Pro	
			260					265					270			
Ser	Ala	Gly	Arg	Leu	Asn	Val	Asp	Val	Ile	Arg	Ala	Lys	Gln	Leu	Leu	
			275				280					285				
Gln	Thr	Asp	Val	Ser	Gln	Gly	Ser	Asp	Pro	Phe	Val	Lys	Ile	Gln	Leu	
			290			295					300					
Val	His	Gly	Leu	Lys	Leu	Val	Lys	Thr	Lys	Lys	Thr	Ser	Phe	Leu	Arg	
305				310						315					320	
Gly	Thr	Ile	Asp	Pro	Phe	Tyr	Asn	Glu	Ser	Phe	Ser	Phe	Lys	Val	Pro	
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 <222> 1879..1894

<400> 27

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ctg gct ctt ctt tca gcg ttt tcg gcc acc cag gca cgg aaa ggc ttc    101
Leu Ala Leu Leu Ser Ala Phe Ser Ala Thr Gln Ala Arg Lys Gly Phe
      -10                                -5                                1

tgg gac tac ttc agc cag acc agc ggg gac aaa ggc agg gtg gag cag    149
Trp Asp Tyr Phe Ser Gln Thr Ser Gly Asp Lys Gly Arg Val Glu Gln
5      10      15      20

atc cat cag cag aag atg gct cgc gag ccc gcg acc ctg aaa gac agc    197
Ile His Gln Gln Lys Met Ala Arg Glu Pro Ala Thr Leu Lys Asp Ser
      25      30      35

ctt gag caa gac ctc aac aat atg aac aag ttc ctg gaa aag ctg agg    245
Leu Glu Gln Asp Leu Asn Asn Met Asn Lys Phe Leu Glu Lys Leu Arg
      40      45      50

cct ctg agt ggg agc gag gct cct cgg ctc cca cag gac ccg gtg ggc    293
Pro Leu Ser Gly Ser Glu Ala Pro Arg Leu Pro Gln Asp Pro Val Gly
      55      60      65

atg cgg cgg cag ctg cag gag gag ttg gag gag gtg aag gct cgc ctc    341
Met Arg Arg Gln Leu Gln Glu Glu Leu Glu Glu Val Lys Ala Arg Leu
      70      75      80

cag ccc tac atg gca gag gcg cac gag ctg gtg ggc tgg aat ttg gag    389
Gln Pro Tyr Met Ala Glu Ala His Glu Leu Val Gly Trp Asn Leu Glu
      85      90      95      100

ggc ttg cgg cag caa ctg aag ccc tac acg atg gat ctg atg gag cag    437
Gly Leu Arg Gln Leu Lys Pro Tyr Thr Met Asp Leu Met Glu Gln
      105      110      115

gtg gcc ctg cgc gtg cag gag ctg cag gag cag ttg cgc gtg gtg ggg    485
Val Ala Leu Arg Val Gln Glu Leu Gln Glu Gln Leu Arg Val Val Gly
      120      125      130

gaa gac acc aag gcc cag ttg ctg ggg ggc gtg gac gag gct tgg gct    533
Glu Asp Thr Lys Ala Gln Leu Leu Gly Gly Val Asp Glu Ala Trp Ala
      135      140      145

ttg ctg cag gga ctg cag agc cgc gtg gtg cac cac acc ggc cgc ttc    581
Leu Leu Gln Gly Leu Gln Ser Arg Val Val His His Thr Gly Arg Phe
      150      155      160

aaa gag ctc ttc cac cca tac gcc gag agc ctg gtg agc ggc atc ggg    629
Lys Glu Leu Phe His Pro Tyr Ala Glu Ser Leu Val Ser Gly Ile Gly
      165      170      175      180

cgc cac gtg cag gag ctg cac cgc agt gtg gct ccg cac gcc ccc gcc    677
Arg His Val Gln Glu Leu His Arg Ser Val Ala Pro His Ala Pro Ala
      185      190      195

agc ccc gcg cgc ctc agt cgc tgc gtg cag gtg ctc tcc cgg aag ctc    725
Ser Pro Ala Arg Leu Ser Arg Cys Val Gln Val Leu Ser Arg Lys Leu
      200      205      210

acg ctc aag gcc aag gcc ctg cac gca cgc atc cag cag aac ctg gac    773
Thr Leu Lys Ala Lys Ala Leu His Ala Arg Ile Gln Gln Asn Leu Asp
      215      220      225

cag ctg cgc gaa gag ctc agc aga gcc ttt gca ggc act ggg act gag    821

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097646104504



Asn	Asn	Met	Asn	Lys	Phe	Leu	Glu	Lys	Leu	Arg	Pro	Leu	Ser	Gly	Ser
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Glu	Ala	Pro	Arg	Leu	Pro	Gln	Asp	Pro	Val	Gly	Met	Arg	Arg	Gln	Leu
		60					65					70			
Gln	Glu	Glu	Leu	Glu	Glu	Val	Lys	Ala	Arg	Leu	Gln	Pro	Tyr	Met	Ala
		75				80					85				
Glu	Ala	His	Glu	Leu	Val	Gly	Trp	Asn	Leu	Glu	Gly	Leu	Arg	Gln	Gln
90					95					100				105	
Leu	Lys	Pro	Tyr	Thr	Met	Asp	Leu	Met	Glu	Gln	Val	Ala	Leu	Arg	Val
				110					115					120	
Gln	Glu	Leu	Gln	Glu	Gln	Leu	Arg	Val	Val	Gly	Glu	Asp	Thr	Lys	Ala
			125					130					135		
Gln	Leu	Leu	Gly	Gly	Val	Asp	Glu	Ala	Trp	Ala	Leu	Leu	Gln	Gly	Leu
		140					145					150			
Gln	Ser	Arg	Val	Val	His	His	Thr	Gly	Arg	Phe	Lys	Glu	Leu	Phe	His
		155				160					165				
Pro	Tyr	Ala	Glu	Ser	Leu	Val	Ser	Gly	Ile	Gly	Arg	His	Val	Gln	Glu
170					175					180					185
Leu	His	Arg	Ser	Val	Ala	Pro	His	Ala	Pro	Ala	Ser	Pro	Ala	Arg	Leu
				190					195					200	
Ser	Arg	Cys	Val	Gln	Val	Leu	Ser	Arg	Lys	Leu	Thr	Leu	Lys	Ala	Lys
			205					210					215		
Ala	Leu	His	Ala	Arg	Ile	Gln	Gln	Asn	Leu	Asp	Gln	Leu	Arg	Glu	Glu
		220					225					230			
Leu	Ser	Arg	Ala	Phe	Ala	Gly	Thr	Gly	Thr	Glu	Glu	Gly	Ala	Gly	Pro
		235				240					245				
Asp	Pro	Gln	Met	Leu	Ser	Glu	Glu	Val	Arg	Gln	Arg	Leu	Gln	Ala	Phe
250					255					260				265	
Arg	Gln	Asp	Thr	Tyr	Leu	Gln	Ile	Ala	Ala	Phe	Thr	Arg	Ala	Ile	Asp
				270					275					280	
Gln	Glu	Thr	Glu	Glu	Val	Gln	Gln	Gln	Leu	Ala	Pro	Pro	Pro	Pro	Gly
			285					290					295		
His	Ser	Ala	Phe	Ala	Pro	Glu	Phe	Gln	Gln	Thr	Asp	Ser	Gly	Lys	Val
		300					305					310			
Leu	Ser	Lys	Leu	Gln	Ala	Arg	Leu	Asp	Asp	Leu	Trp	Glu	Asp	Ile	Thr
		315				320					325				
His	Ser	Leu	His	Asp	Gln	Gly	His	Ser	His	Leu	Gly	Asp	Pro		
330					335					340					

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<222> 728..742

<400> 29

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Pro Ser Thr Asp Ser Gly Lys Glu Glu Tyr Ile Ala Thr Phe Lys Gly
      10      15      20
tct gaa tac ttc tgc tac gac ttg tct caa aac ccc att caa agc agc      148
Ser Glu Tyr Phe Cys Tyr Asp Leu Ser Gln Asn Pro Ile Gln Ser Ser
      25      30      35
agt gat gaa ata act ctg tca ttt aaa acc ctt cag agg aat gga ctg      196
Ser Asp Glu Ile Thr Leu Ser Phe Lys Thr Leu Gln Arg Asn Gly Leu
      40      45      50      55
atg ctt cac act ggg aaa tcg gct gat tat gtc aat ctt gcc ctg aaa      244
Met Leu His Thr Gly Lys Ser Ala Asp Tyr Val Asn Leu Ala Leu Lys
      60      65      70
aat gga gct gtc tct ctg gtc att aat ttg gga tca ggg gcc ttt gaa      292
Asn Gly Ala Val Ser Leu Val Ile Asn Leu Gly Ser Gly Ala Phe Glu
      75      80      85
gca cta gtg gag cct gtg aat gga aag ttt aat gat aat gcc tgg cat      340
Ala Leu Val Glu Pro Val Asn Gly Lys Phe Asn Asp Asn Ala Trp His
      90      95      100
gat gtg aaa gtc acc agg aat ctg cgt cag gtg aca ata tca gtg gat      388
Asp Val Lys Val Thr Arg Asn Leu Arg Gln Val Thr Ile Ser Val Asp
      105      110      115
ggg att ctt acc aca acg ggc tac acg caa gaa gat tat acc atg ctg      436
Gly Ile Leu Thr Thr Thr Gly Tyr Thr Gln Glu Asp Tyr Thr Met Leu
      120      125      130      135
ggg tct gat gac ttt ttc tat gtt gga ggc agt ccc agc aca gcc gac      484
Gly Ser Asp Asp Phe Phe Tyr Val Gly Gly Ser Pro Ser Thr Ala Asp
      140      145      150
ctt cca ggg tca cca atc cag cat gaa agc acc ttt gct gaa gac ccg      532
Leu Pro Gly Ser Pro Ile Gln His Glu Ser Thr Phe Ala Glu Asp Pro
      155      160      165
atg ttc cag agt caa acg gca caa ctt taaattcaat attctactat      579
Met Phe Gln Ser Gln Thr Ala Gln Leu
      170      175
tgtttatgta ggattggggg agggaaacag ctcatagatc attatgaagg aattaggttc 639
ctcttcttta ttagtctgta agtaatttac atttgagatt tgtgtggaca gttgatatta 699
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<210> 30

<211> 176

<212> PRT



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Arg	Val	Ser	Asp	Leu	Gln	Met	Leu	Leu	Gly	Phe	Val	Gly	Arg	Ser	Lys	
20				25				30								
agt	gga	ctg	aag	cac	gag	ctc	gtc	acc	agg	gcc	ctc	cag	ctg	gtg	cag	144
Ser	Gly	Leu	Lys	His	Glu	Leu	Val	Thr	Arg	Ala	Leu	Gln	Leu	Val	Gln	
35				40				45								
ttt	gac	tgt	acc	cct	gag	ctg	ttc	aag	aag	atc	aag	gag	ctg	tac	gag	192
Phe	Asp	Cys	Thr	Pro	Glu	Leu	Phe	Lys	Lys	Ile	Lys	Glu	Leu	Tyr	Glu	
50				55				60								
acc	cgc	tac	gcc	aag	aag	aac	tcg	gag	cct	gcc	cca	cag	ccg	cac	cgg	240
Thr	Arg	Tyr	Ala	Lys	Lys	Asn	Ser	Glu	Pro	Ala	Pro	Gln	Pro	His	Arg	
65				70				75								
ccc	ctg	gac	ccc	ctg	acc	atg	cac	tcc	acc	tac	gac	cgg	gcc	ggc	gct	288
Pro	Leu	Asp	Pro	Leu	Thr	Met	His	Ser	Thr	Tyr	Asp	Arg	Ala	Gly	Ala	
80				85				90				95				
gtg	ccc	agg	act	ccg	ctg	gca	ggc	ccc	aat	att	gac	tac	ccc	gtg	ctc	336
Val	Pro	Arg	Thr	Pro	Leu	Ala	Gly	Pro	Asn	Ile	Asp	Tyr	Pro	Val	Leu	
100				105				110								
tac	gga	aag	tac	tta	aac	gga	ctg	gga	cgg	ttg	ccc	gcc	aag	acc	ctc	384
Tyr	Gly	Lys	Tyr	Leu	Asn	Gly	Leu	Gly	Arg	Leu	Pro	Ala	Lys	Thr	Leu	
115				120				125								
aag	cca	gaa	gtc	cgc	ctg	gtg	aag	ctg	ccg	ttc	ttt	aat	atg	ctg	gac	432
Lys	Pro	Glu	Val	Arg	Leu	Val	Lys	Leu	Pro	Phe	Phe	Asn	Met	Leu	Asp	
130				135				140								
gag	ctg	ctg	aag	ccc	acc	gaa	tta	gtc	cca	cag	aac	aac	gag	aag	ctt	480
Glu	Leu	Leu	Lys	Pro	Thr	Glu	Leu	Val	Pro	Gln	Asn	Asn	Glu	Lys	Leu	
145				150				155								
cag	gag	agc	ccg	tgc	atc	ttc	gca	ttg	acg	cca	aga	cag	gtg	gag	ttg	528
Gln	Glu	Ser	Pro	Cys	Ile	Phe	Ala	Leu	Thr	Pro	Arg	Gln	Val	Glu	Leu	
160				165				170				175				
atc	cgg	aac	tcc	agg	gaa	ctg	cag	ccc	gga	gtt	aaa	gcc	gtg	cag	gtc	576
Ile	Arg	Asn	Ser	Arg	Glu	Leu	Gln	Pro	Gly	Val	Lys	Ala	Val	Gln	Val	
180				185				190								
gtc	ctg	aga	atc	tgt	tac	tca	gac	acc	agc	tgc	cct	cag	gag	gac	cag	624
Val	Leu	Arg	Ile	Cys	Tyr	Ser	Asp	Thr	Ser	Cys	Pro	Gln	Glu	Asp	Gln	
195				200				205								
tac	ccg	ccc	aac	atc	gct	gtg	aag	gtc	aac	cac	agc	tac	tgc	tcc	gtc	672
Tyr	Pro	Pro	Asn	Ile	Ala	Val	Lys	Val	Asn	His	Ser	Tyr	Cys	Ser	Val	
210				215				220								
ccg	ggc	tac	tac	ccc	tcc	aat	aag	ccc	ggg	gtg	gag	ccc	aag	agg	ccg	720
Pro	Gly	Tyr	Tyr	Pro	Ser	Asn	Lys	Pro	Gly	Val	Glu	Pro	Lys	Arg	Pro	
225				230				235								
tgc	cgc	ccc	atc	aac	ctc	acc	cac	ctc	atg	tac	ctt	tcc	tcg	gcc	acc	768
Cys	Arg	Pro	Ile	Asn	Leu	Thr	His	Leu	Met	Tyr	Leu	Ser	Ser	Ala	Thr	
240				245				250				255				
aac	cgc	atc	act	gtc	acc	tgg	ggg	aac								

290	295	300	
aag gag aag ctg cgc ctt gat cct gac agc gag atc gcc acc acc ggt			960
Lys Glu Lys Leu Arg Leu Asp Pro Asp Ser Glu Ile Ala Thr Thr Gly			
305	310	315	
gtg cgg gtg tcc ctc atc tgt ccg ctg gtg aag atg cgg ctc tcc gtg			1008
Val Arg Val Ser Leu Ile Cys Pro Leu Val Lys Met Arg Leu Ser Val			
320	325	330	335
ccc tgc cgg gca gag acc tgc gcc cac ctg cag tgc ttc gac gcc gtc			1056
Pro Cys Arg Ala Glu Thr Cys Ala His Leu Gln Cys Phe Asp Ala Val			
340	345	350	
ttc tac ctg cag atg aac gag aag aag ccc acc tgg atg tgc ccc gtg			1104
Phe Tyr Leu Gln Met Asn Glu Lys Lys Pro Thr Trp Met Cys Pro Val			
355	360	365	
tgc gac aag cca gcc ccc tac gac cag ctc atc atc gac ggg ctc ctc			1152
Cys Asp Lys Pro Ala Pro Tyr Asp Gln Leu Ile Ile Asp Gly Leu Leu			
370	375	380	
tcg aag atc ctg agc gag tgt gag gac gcc gac gag atc gag tac ctg			1200
Ser Lys Ile Leu Ser Glu Cys Glu Asp Ala Asp Glu Ile Glu Tyr Leu			
385	390	395	
gtg gac ggc tcg tgg tgc ccg atc cgc gcc gaa aag gag ctc agc tgc			1248
Val Asp Gly Ser Trp Cys Pro Ile Arg Ala Glu Lys Glu Leu Ser Cys			
400	405	410	415
agc ccg cag ggc gcc atc ctc gtg ctg ggc ccc tcg gac gcc aat ggg			1296
Ser Pro Gln Gly Ala Ile Leu Val Leu Gly Pro Ser Asp Ala Asn Gly			
420	425	430	
ctc ctg ccc gcc ccc agc gtc aac ggg agc ggt gcc ctg ggc agc acg			1344
Leu Leu Pro Ala Pro Ser Val Asn Gly Ser Gly Ala Leu Gly Ser Thr			
435	440	445	
ggt ggc ggc ggc ccg gtg ggc agc atg gag aat ggg aag ccg ggc gcc			1392
Gly Gly Gly Gly Pro Val Gly Ser Met Glu Asn Gly Lys Pro Gly Ala			
450	455	460	
gat gtg gtg gac ctc acg ctg gac agc tca tcg tcc tcg gag gat gag			1440
Asp Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu			
465	470	475	
gag gag gag gaa gag gag gag gaa gac gag gac gaa gag ggg ccc cgg			1488
Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg			
480	485	490	495
ccc aag cgc cgc tgc ccc ttc cag aag ggc ctg gtg ccg gcc tgc			1533
Pro Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys			
500	505	510	
tgaccccgcc cgcacacttg actttcctgg tgctcaccac gcagagggggc acggggccagc			1593
ctcgggcgca gagggaggag tgacctttct ttttcctttt attgtcgttc gttttgtttt			1653
tccacccttt tgccctggctc ctggcacctg tacctctgga ctctcctatc gggggattaa			1713
aaaaaaaaagt aaaatgacaa aaaaagatac aaaaaagaaa aaaaaaaaaa aaa			1766

<210> 32

<211> 510

<212> PRT

<213> Homo sapiens

<400> 32

Met	Ala	Ala	Glu	Leu	Val	Glu	Ala	Lys	Asn	Met	Val	Met	Ser	Phe	Arg
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Val	Ser	Asp	Leu	Gln	Met	Leu	Leu	Gly	Phe	Val	Gly	Arg	Ser	Lys	Ser

				20				25					30		
Gly	Leu	Lys	His	Glu	Leu	Val	Thr	Arg	Ala	Leu	Gln	Leu	Val	Gln	Phe
		35					40					45			
Asp	Cys	Thr	Pro	Glu	Leu	Phe	Lys	Lys	Ile	Lys	Glu	Leu	Tyr	Glu	Thr
	50					55					60				
Arg	Tyr	Ala	Lys	Lys	Asn	Ser	Glu	Pro	Ala	Pro	Gln	Pro	His	Arg	Pro
65					70					75					80
Leu	Asp	Pro	Leu	Thr	Met	His	Ser	Thr	Tyr	Asp	Arg	Ala	Gly	Ala	Val
				85					90					95	
Pro	Arg	Thr	Pro	Leu	Ala	Gly	Pro	Asn	Ile	Asp	Tyr	Pro	Val	Leu	Tyr
			100					105					110		
Gly	Lys	Tyr	Leu	Asn	Gly	Leu	Gly	Arg	Leu	Pro	Ala	Lys	Thr	Leu	Lys
		115					120					125			
Pro	Glu	Val	Arg	Leu	Val	Lys	Leu	Pro	Phe	Phe	Asn	Met	Leu	Asp	Glu
	130					135						140			
Leu	Leu	Lys	Pro	Thr	Glu	Leu	Val	Pro	Gln	Asn	Asn	Glu	Lys	Leu	Gln
145					150					155					160
Glu	Ser	Pro	Cys	Ile	Phe	Ala	Leu	Thr	Pro	Arg	Gln	Val	Glu	Leu	Ile
				165					170					175	
Arg	Asn	Ser	Arg	Glu	Leu	Gln	Pro	Gly	Val	Lys	Ala	Val	Gln	Val	Val
			180					185					190		
Leu	Arg	Ile	Cys	Tyr	Ser	Asp	Thr	Ser	Cys	Pro	Gln	Glu	Asp	Gln	Tyr
		195					200					205			
Pro	Pro	Asn	Ile	Ala	Val	Lys	Val	Asn	His	Ser	Tyr	Cys	Ser	Val	Pro
	210					215						220			
Gly	Tyr	Tyr	Pro	Ser	Asn	Lys	Pro	Gly	Val	Glu	Pro	Lys	Arg	Pro	Cys
225					230					235					240
Arg	Pro	Ile	Asn	Leu	Thr	His	Leu	Met	Tyr	Leu	Ser	Ser	Ala	Thr	Asn
			245						250					255	
Arg	Ile	Thr	Val	Thr	Trp	Gly	Asn	Tyr	Gly	Lys	Ser	Tyr	Ser	Val	Ala
			260				265						270		
Leu	Tyr	Leu	Val	Arg	Gln	Leu	Thr	Ser	Ser	Glu	Leu	Leu	Gln	Arg	Leu
		275					280					285			
Lys	Thr	Ile	Gly	Val	Lys	His	Pro	Glu	Leu	Cys	Lys	Ala	Leu	Val	Lys
	290					295					300				
Glu	Lys	Leu	Arg	Leu	Asp	Pro	Asp	Ser	Glu	Ile	Ala	Thr	Thr	Gly	Val
305					310					315					320
Arg	Val	Ser	Leu	Ile	Cys	Pro	Leu	Val	Lys	Met	Arg	Leu	Ser	Val	Pro
			325						330					335	
Cys	Arg	Ala	Glu	Thr	Cys	Ala	His	Leu	Gln	Cys	Phe	Asp	Ala	Val	Phe
			340					345					350		
Tyr	Leu	Gln	Met	Asn	Glu	Lys	Lys	Pro	Thr	Trp	Met	Cys	Pro	Val	Cys
		355					360					365			
Asp	Lys	Pro	Ala	Pro	Tyr	Asp	Gln	Leu	Ile	Ile	Asp	Gly	Leu	Leu	Ser



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      450              455              460
Val Val Asp Leu Thr Leu Asp Ser Ser Ser Ser Ser Glu Asp Glu Glu
465              470              475              480
Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Glu Gly Pro Arg Pro
      485              490              495
Lys Arg Arg Cys Pro Phe Gln Lys Gly Leu Val Pro Ala Cys
      500              505              510

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<210> 33
<211> 877
<212> DNA
<213> Homo sapiens

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<220>
<221> 5'UTR
<222> 1..10

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<220>
<221> CDS
<222> 11..802

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<220>
<221> 3'UTR
<222> 803..877

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<220>
<221> polyA_signal
<222> 836..841

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<220>
<221> polyA_site
<222> 862..877

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<400> 33
atctgccacg atg ttg ctg ctc agc ctg acc cta agc ctg gtt ctc ctc      49
      Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu
      -15              -10
ggc tcc tcc tgg ggc tgc ggc att cct gcc atc aaa ccg gca ctg agc      97
Gly Ser Ser Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser
-5              1              5              10
ttc agc cag agg att gtc aac ggg gag aat gca gtg ttg ggc tcc tgg      145
Phe Ser Gln Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp
      15              20              25
ccc tgg cag gtg tcc ctg cag gac agc agc gac ttc cac ttc tgc ggt      193
Pro Trp Gln Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly
      30              35              40
ggt tct ctc atc agc cag tcc tgg gtg gtc act gct gcc cac tgc aat      241
Gly Ser Leu Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn
      45              50              55
gtc agc cct ggc cgc cat ttt gtt gtc ctg ggc gag tat gac cga tca      289
Val Ser Pro Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser
      60              65              70              75
tca aac gca gag ccc ttg cag gtt ctg tcc gtc tct cgg gcc att aca      337
Ser Asn Ala Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr

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	80		85		90	
cac cct agc tgg aac tct acc acc atg aac aat gac gtg acg ctg ctg	385					
His Pro Ser Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu						
95 100 105						
aag ctc gcc tcg cca gcc cag tac aca aca cgc atc tcg cca gtt tgc	433					
Lys Leu Ala Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys						
110 115 120						
ctg gca tcc tca aac gag gct ctg act gaa ggc ctc acg tgt gtc acc	481					
Leu Ala Ser Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr						
125 130 135						
acc ggc tgg ggt cgc ctc agt ggc gtg ggc aat gtg aca cca gca cgt	529					
Thr Gly Trp Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala Arg						
140 145 150 155						
ctg cag cag gtg gct ttg ccc ctg gtc act gtg aat cag tgc cgg cag	577					
Leu Gln Gln Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln						
160 165 170						
tac tgg ggc tca agt atc act gac tcc atg atc tgt gca ggt ggc gca	625					
Tyr Trp Gly Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala						
175 180 185						
ggc gcc tcc tcg tgc cag ggt gac tcc gga ggc cct ctt gtc tgc cag	673					
Gly Ala Ser Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln						
190 195 200						
aag gga aac aca tgg gtg ctt att ggt att gtc tcc tgg ggc acc aaa	721					
Lys Gly Asn Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys						
205 210 215						
aac tgc aat gtg cgc gca cct gct gtg tat act cga gtt agc aag ttc	769					
Asn Cys Asn Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe						
220 225 230 235						
agc acc tgg atc aac cag gtc ata gcc tac aac tgagctcacc acaggccctc	822					
Ser Thr Trp Ile Asn Gln Val Ile Ala Tyr Asn						
240 245						
cccagctcaa cccattaaag acccaggccc tgtcccatca aaaaaaaaaa aaaaa	877					

<210> 34  
 <211> 264  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..18

<400> 34  
 Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser  
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 Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln  
 1 5 10  
 Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln  
 15 20 25 30  
 Val Ser Leu Gln Asp Ser Ser Asp Phe His Phe Cys Gly Gly Ser Leu  
 35 40 45  
 Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro  
 50 55 60  
 Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala

		65					70					75			
Glu	Pro	Leu	Gln	Val	Leu	Ser	Val	Ser	Arg	Ala	Ile	Thr	His	Pro	Ser
	80					85					90				
Trp	Asn	Ser	Thr	Thr	Met	Asn	Asn	Asp	Val	Thr	Leu	Leu	Lys	Leu	Ala
95					100					105					110
Ser	Pro	Ala	Gln	Tyr	Thr	Thr	Arg	Ile	Ser	Pro	Val	Cys	Leu	Ala	Ser
				115					120					125	
Ser	Asn	Glu	Ala	Leu	Thr	Glu	Gly	Leu	Thr	Cys	Val	Thr	Thr	Gly	Trp
			130					135					140		
Gly	Arg	Leu	Ser	Gly	Val	Gly	Asn	Val	Thr	Pro	Ala	Arg	Leu	Gln	Gln
		145					150					155			
Val	Ala	Leu	Pro	Leu	Val	Thr	Val	Asn	Gln	Cys	Arg	Gln	Tyr	Trp	Gly
	160					165					170				
Ser	Ser	Ile	Thr	Asp	Ser	Met	Ile	Cys	Ala	Gly	Gly	Ala	Gly	Ala	Ser
175					180					185					190
Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gln	Lys	Gly	Asn
				195					200					205	
Thr	Trp	Val	Leu	Ile	Gly	Ile	Val	Ser	Trp	Gly	Thr	Lys	Asn	Cys	Asn
		210						215					220		
Val	Arg	Ala	Pro	Ala	Val	Tyr	Thr	Arg	Val	Ser	Lys	Phe	Ser	Thr	Trp
		225					230					235			
Ile	Asn	Gln	Val	Ile	Ala	Tyr	Asn								
	240					245									

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<210> 35
<211> 1728
<212> DNA
<213> Homo sapiens
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<220>  
<221> 5' UTR  
<222> 1..37

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<220>
<221> CDS
<222> 38..1378
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<220>  
<221> 3'UTR  
<222> 1379..1728

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<220>
<221> polyA_site
<222> 1713..1728
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<400> 35
atcatctgca cagctggggc ccctgggagg agacgcc atg atc ccc acc ttc acg      55
                                     Met Ile Pro Thr Phe Thr
                                     -20
gct ctg ctc tgc ctc ggg ctg agt ctg ggc ccc agg acc cac atg cag      103
Ala Leu Leu Cys Leu Gly Leu Ser Leu Gly Pro Arg Thr His Met Gln
      -15                                -10                                -5
gca ggg ccc ctc ccc aaa ccc acc ctc tgg gct gag cca ggc tct gtg      151
Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp Ala Glu Pro Gly Ser Val

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	1			5			10			15						
atc	agc	tgg	ggg	aac	tct	gtg	acc	atc	tgg	tgt	cag	ggg	acc	ctg	gag	199
Ile	Ser	Trp	Gly	Asn	Ser	Val	Thr	Ile	Trp	Cys	Gln	Gly	Thr	Leu	Glu	
				20					25					30		
gct	cgg	gag	tac	cgt	ctg	gat	aaa	gag	gaa	agc	cca	gca	ccc	tgg	gac	247
Ala	Arg	Glu	Tyr	Arg	Leu	Asp	Lys	Glu	Glu	Ser	Pro	Ala	Pro	Trp	Asp	
			35					40					45			
aga	cag	aac	cca	ctg	gag	ccc	aag	aac	aag	gcc	aga	ttc	tcc	atc	cca	295
Arg	Gln	Asn	Pro	Leu	Glu	Pro	Lys	Asn	Lys	Ala	Arg	Phe	Ser	Ile	Pro	
			50				55					60				
tcc	atg	aca	gag	gac	tat	gca	ggg	aga	tac	cgc	tgt	tac	tat	cgc	agc	343
Ser	Met	Thr	Glu	Asp	Tyr	Ala	Gly	Arg	Tyr	Arg	Cys	Tyr	Tyr	Arg	Ser	
	65					70				75						
cct	gta	ggc	tgg	tca	cag	ccc	agt	gac	ccc	ctg	gag	ctg	gtg	atg	aca	391
Pro	Val	Gly	Trp	Ser	Gln	Pro	Ser	Asp	Pro	Leu	Glu	Leu	Val	Met	Thr	
	80				85					90					95	
gga	gcc	tac	agt	aaa	ccc	acc	ctt	tca	gcc	ctg	ccg	agt	cct	ctt	gtg	439
Gly	Ala	Tyr	Ser	Lys	Pro	Thr	Leu	Ser	Ala	Leu	Pro	Ser	Pro	Leu	Val	
				100						105				110		
acc	tca	gaa	aag	agc	gtg	acc	ctg	ctg	tgt	cag	tca	cgg	agc	cca	atg	487
Thr	Ser	Glu	Lys	Ser	Val	Thr	Leu	Leu	Cys	Gln	Ser	Arg	Ser	Pro	Met	
			115					120					125			
gac	act	ttc	ctt	ctg	atc	aag	gag	cgg	gca	gcc	cat	ccc	cta	ctg	cat	535
Asp	Thr	Phe	Leu	Leu	Ile	Lys	Glu	Arg	Ala	Ala	His	Pro	Leu	Leu	His	
		130					135					140				
ctg	aga	tca	gag	cac	gga	gct	cag	cag	cac	cag	gct	gaa	ttc	ccc	atg	583
Leu	Arg	Ser	Glu	His	Gly	Ala	Gln	Gln	His	Gln	Ala	Glu	Phe	Pro	Met	
	145					150					155					
agt	cct	gtg	acc	tca	gtg	cac	ggg	ggg	acc	tac	agg	tgc	ttc	agc	tca	631
Ser	Pro	Val	Thr	Ser	Val	His	Gly	Gly	Thr	Tyr	Arg	Cys	Phe	Ser	Ser	
	160				165					170					175	
cac	ggc	ttc	tcc	cac	tac	ctg	ctg	tca	cac	ccc	agt	gac	ccc	ctg	gag	679
His	Gly	Phe	Ser	His	Tyr	Leu	Leu	Ser	His	Pro	Ser	Asp	Pro	Leu	Glu	
				180						185				190		
ctc	ata	gtc	tca	gga	tcc	ttg	gag	gat	ccc	agg	ccc	tca	ccc	aca	agg	727
Leu	Ile	Val	Ser	Gly	Ser	Leu	Glu	Asp	Pro	Arg	Pro	Ser	Pro	Thr	Arg	
			195					200					205			
tcc	gtc	tca	aca	gct	gca	ggc	cct	gag	gac	cag	ccc	ctc	atg	cct	aca	775
Ser	Val	Ser	Thr	Ala	Ala	Gly	Pro	Glu	Asp	Gln	Pro	Leu	Met	Pro	Thr	
		210					215					220				
ggg	tca	gtc	ccc	cac	agt	ggt	ctg	aga	agg	cac	tgg	gag	gta	ctg	atc	823
Gly	Ser	Val	Pro	His	Ser	Gly	Leu	Arg	Arg	His	Trp	Glu	Val	Leu	Ile	
	225					230					235					
ggg	gtc	ttg	gtg	gtc	tcc	atc	ctg	ctt	ctc	tcc	ctc	ctc	ctc	ttc	ctc	871
Gly	Val	Leu	Val	Val	Ser	Ile	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Phe	Leu	
	240				245					250					255	
ctc	ctc	caa	cac	tgg	cgt	cag	gga	aaa	cac	agg	aca	ttg	gcc	cag	aga	919
Leu	Leu	Gln	His	Trp	Arg	Gln	Gly	Lys	His	Arg	Thr	Leu	Ala	Gln	Arg	
			260					265					270			
cag	gct	gat	ttc	caa	cgt	cct	cca	ggg	gct	gcc	gag	cca	gag	ccc	aag	967
Gln	Ala	Asp	Phe	Gln	Arg	Pro	Pro	Gly	Ala	Ala	Glu	Pro	Glu	Pro	Lys	
			275					280					285			
gac	ggg	ggc	cta	cag	agg	agg	tcc	agc	cca	gct	gct	gac	gtc	cag	gga	1015
Asp	Gly	Gly	Leu	Gln	Arg	Arg	Ser	Ser	Pro	Ala	Ala	Asp	Val	Gln	Gly	

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Glu Asn Phe Cys Ala Ala Val Lys Asp Thr Gln Pro Glu Asp Gly Val
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gaa atg gac act cgg agc cca cac gat gaa gac ccc cag gca gtg acg 1111
Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr
      320              325              330              335
tat gcc aag gtg aaa cac tcc aga cct agg aga gaa atg gcc tct cct 1159
Tyr Ala Lys Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro
      340              345              350
ccc tcc cca ctg tct ggg gaa ttc ctg gac aca aag gac aga cag gca 1207
Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala
      355              360              365
gaa gag gac aga cag atg gac act gag gct gct gca tct gaa gcc ccc 1255
Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro
      370              375              380
cag gat gtg acc tac gcc cag ctg cac agc ttt acc ctc aga cag aag 1303
Gln Asp Val Thr Tyr Ala Gln Leu His Ser Phe Thr Leu Arg Gln Lys
      385              390              395
gca act gag cct cct cca tcc cag gaa ggg gcc tct cca gct gag ccc 1351
Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Ala Ser Pro Ala Glu Pro
      400              405              410              415
agt gtc tat gcc act ctg gcc atc cac taatccaggg gggacccaga 1398
Ser Val Tyr Ala Thr Leu Ala Ile His
      420
ccccacaagc catggagact caggaccccca gaaggcatgg aagctgcctc cagtagacat 1458
cactgaaccc cagccagccc agacccttga cacagaccac tagaagattc cggaacggtt 1518
gggagtcacc tgattctgca aagataaata atatccctgc attatcaaaa taaagtagca 1578
gacctctcaa ttcacaatga gttaactgat aaaacaaaac agaagtcaga caatgtttta 1638
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taatgaggac aaacaaaaaa aaaaaaaaaa 1728

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<210> 36  
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 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> 1..23

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Pro Arg Thr His Met Gln Ala Gly Pro Leu Pro Lys Pro Thr Leu Trp
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Ala Glu Pro Gly Ser Val Ile Ser Trp Gly Asn Ser Val Thr Ile Trp
      10              15              20              25
Cys Gln Gly Thr Leu Glu Ala Arg Glu Tyr Arg Leu Asp Lys Glu Glu
      30              35              40
Ser Pro Ala Pro Trp Asp Arg Gln Asn Pro Leu Glu Pro Lys Asn Lys
      45              50              55
Ala Arg Phe Ser Ile Pro Ser Met Thr Glu Asp Tyr Ala Gly Arg Tyr
      60              65              70

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Arg	Cys	Tyr	Tyr	Arg	Ser	Pro	Val	Gly	Trp	Ser	Gln	Pro	Ser	Asp	Pro
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Leu	Glu	Leu	Val	Met	Thr	Gly	Ala	Tyr	Ser	Lys	Pro	Thr	Leu	Ser	Ala
90					95					100					105
Leu	Pro	Ser	Pro	Leu	Val	Thr	Ser	Glu	Lys	Ser	Val	Thr	Leu	Leu	Cys
					110					115					120
Gln	Ser	Arg	Ser	Pro	Met	Asp	Thr	Phe	Leu	Leu	Ile	Lys	Glu	Arg	Ala
					125			130					135		
Ala	His	Pro	Leu	Leu	His	Leu	Arg	Ser	Glu	His	Gly	Ala	Gln	Gln	His
		140					145					150			
Gln	Ala	Glu	Phe	Pro	Met	Ser	Pro	Val	Thr	Ser	Val	His	Gly	Gly	Thr
		155				160					165				
Tyr	Arg	Cys	Phe	Ser	Ser	His	Gly	Phe	Ser	His	Tyr	Leu	Leu	Ser	His
170						175				180					185
Pro	Ser	Asp	Pro	Leu	Glu	Leu	Ile	Val	Ser	Gly	Ser	Leu	Glu	Asp	Pro
					190					195					200
Arg	Pro	Ser	Pro	Thr	Arg	Ser	Val	Ser	Thr	Ala	Ala	Gly	Pro	Glu	Asp
					205				210						
Gln	Pro	Leu	Met	Pro	Thr	Gly	Ser	Val	Pro	His	Ser	Gly	Leu	Arg	Arg
		220					225					230			
His	Trp	Glu	Val	Leu	Ile	Gly	Val	Leu	Val	Val	Ser	Ile	Leu	Leu	Leu
		235				240					245				
Ser	Leu	Leu	Leu	Phe	Leu	Leu	Leu	Gln	His	Trp	Arg	Gln	Gly	Lys	His
250					255					260					265
Arg	Thr	Leu	Ala	Gln	Arg	Gln	Ala	Asp	Phe	Gln	Arg	Pro	Pro	Gly	Ala
					270				275						280
Ala	Glu	Pro	Glu	Pro	Lys	Asp	Gly	Gly	Leu	Gln	Arg	Arg	Ser	Ser	Pro
					285			290					295		
Ala	Ala	Asp	Val	Gln	Gly	Glu	Asn	Phe	Cys	Ala	Ala	Val	Lys	Asp	Thr
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Gln	Pro	Glu	Asp	Gly	Val	Glu	Met	Asp	Thr	Arg	Ser	Pro	His	Asp	Glu
						320					325				
Asp	Pro	Gln	Ala	Val	Thr	Tyr	Ala	Lys	Val	Lys	His	Ser	Arg	Pro	Arg
330					335					340					345
Arg	Glu	Met	Ala	Ser	Pro	Pro	Ser	Pro	Leu	Ser	Gly	Glu	Phe	Leu	Asp
					350				355						360
Thr	Lys	Asp	Arg	Gln	Ala	Glu	Glu	Asp	Arg	Gln	Met	Asp	Thr	Glu	Ala
					365			370					375		
Ala	Ala	Ser	Glu	Ala	Pro	Gln	Asp	Val	Thr	Tyr	Ala	Gln	Leu	His	Ser
		380					385					390			
Phe	Thr	Leu	Arg	Gln	Lys	Ala	Thr	Glu	Pro	Pro	Pro	Ser	Gln	Glu	Gly
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Ala	Ser	Pro	Ala	Glu	Pro	Ser	Val	Tyr	Ala	Thr	Leu	Ala	Ile	His	
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<210> 37

<211> 1757

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<213> Homo sapiens

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<220>  
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 cggcccctgg cttgcgctcc cgaagaggag agcaaggctg ttctgggata cggccgtcgt 180  
 gcggcaagag gcttgtctgt ccgggttgcc ggaaccagga gaaccagag ggaaaccgag 240  
 gcaaaggagc ggcgcgtttt actagagaga gcgcgagcgg aagaggcgag agcaggagcg 300  
 cgcgagggag catcgagcgc agcggagac atg agg acc tac tgg ctg cac agc 353  
 Met Arg Thr Tyr Trp Leu His Ser  
 -20  
 gtc tgg gtg ctg ggc ttt ttc ctg tcc ctc ttc tca ttg caa gga ctg 401  
 Val Trp Val Leu Gly Phe Phe Leu Ser Leu Phe Ser Leu Gln Gly Leu  
 -15 -10 -5 1  
 cct gtt cgc agc gtg gat ttt aac cga ggc acg gac aac atc acc gtg 449  
 Pro Val Arg Ser Val Asp Phe Asn Arg Gly Thr Asp Asn Ile Thr Val  
 5 10 15  
 agg cag ggg gac aca gcc atc ctc agg tgc gtt gta gaa gac aag aac 497  
 Arg Gln Gly Asp Thr Ala Ile Leu Arg Cys Val Val Glu Asp Lys Asn  
 20 25 30  
 tca aag gtg gcc tgg ttg aac cgt tct ggc atc att ttt gct gga cat 545  
 Ser Lys Val Ala Trp Leu Asn Arg Ser Gly Ile Ile Phe Ala Gly His  
 35 40 45  
 gac aag tgg tct ctg gac cca cgg gtt gag ctg gag aaa cgc cat tct 593  
 Asp Lys Trp Ser Leu Asp Pro Arg Val Glu Leu Glu Lys Arg His Ser  
 50 55 60 65  
 ctg gaa tac agc ctc cga atc cag aag gtg gat gtc tat gat gag ggt 641  
 Leu Glu Tyr Ser Leu Arg Ile Gln Lys Val Asp Val Tyr Asp Glu Gly  
 70 75 80  
 tcc tac act tgc tca gtt cag aca cag cat gag ccc aag acc tcc caa 689  
 Ser Tyr Thr Cys Ser Val Gln Thr Gln His Glu Pro Lys Thr Ser Gln  
 85 90 95  
 gtt tac ttg atc gta caa gtc cca cca aag atc tcc aat atc tcc tcg 737  
 Val Tyr Leu Ile Val Gln Val Pro Lys Ile Ser Asn Ile Ser Ser  
 100 105 110  
 gat gtc act gtg aat gag ggc agc aac gtg act ctg gtc tgc atg gcc 785  
 Asp Val Thr Val Asn Glu Gly Ser Asn Val Thr Leu Val Cys Met Ala  
 115 120 125  
 aat ggc cgt cct gaa cct gtt atc acc tgg aga cac ctt aca cca act 833  
 Asn Gly Arg Pro Glu Pro Val Ile Thr Trp Arg His Leu Thr Pro Thr

130	135										140					145					
gga agg gaa ttt gaa gga gaa gaa gaa tat ctg gag atc ctt ggc atc	881																				
Gly Arg Glu Phe Glu Gly Glu Glu Glu Tyr Leu Glu Ile Leu Gly Ile																					
	150										155					160					
acc agg gag cag tca ggc aaa tat gag tgc aaa gct gcc aac gag gtc	929																				
Thr Arg Glu Gln Ser Gly Lys Tyr Glu Cys Lys Ala Ala Asn Glu Val																					
	165										170					175					
tcc tcg gcg gat gtc aaa caa gtc aag gtc act gtg aac tat cct ccc	977																				
Ser Ser Ala Asp Val Lys Gln Val Lys Val Thr Val Asn Tyr Pro Pro																					
	180										185					190					
act atc aca gaa tcc aag agc aat gaa gcc acc aca gga cga caa gct	1025																				
Thr Ile Thr Glu Ser Lys Ser Asn Glu Ala Thr Thr Gly Arg Gln Ala																					
	195										200					205					
tca ctc aaa tgt gag gcc tcg gca gtg cct gca cct gac ttt gag tgg	1073																				
Ser Leu Lys Cys Glu Ala Ser Ala Val Pro Ala Pro Asp Phe Glu Trp																					
210	215										220					225					
tac cgg gat gac act agg ata aat agt gcc aat ggc ctt gag att aag	1121																				
Tyr Arg Asp Asp Thr Arg Ile Asn Ser Ala Asn Gly Leu Glu Ile Lys																					
	230										235					240					
agc acg gag ggc cag tct tcc ctg acg gtg acc aac gtc act gag gag	1169																				
Ser Thr Glu Gly Gln Ser Ser Leu Thr Val Thr Asn Val Thr Glu Glu																					
	245										250					255					
cac tac ggc aac tac acc tgt gtg gct gcc aac aag ctg ggg gtc acc	1217																				
His Tyr Gly Asn Tyr Thr Cys Val Ala Ala Asn Lys Leu Gly Val Thr																					
	260										265					270					
aat gcc agc cta gtc ctt ttc aaa cgt gtt tta ccc aca atc ccc cac	1265																				
Asn Ala Ser Leu Val Leu Phe Lys Arg Val Leu Pro Thr Ile Pro His																					
	275										280					285					
ccc att caa gaa att ggt acc acc gtg cac ttc aag caa aaa ggc atc	1313																				
Pro Ile Gln Glu Ile Gly Thr Thr Val His Phe Lys Gln Lys Gly Ile																					
290	295										300					305					
ttc ctc tct gag tct cag agg ggt gag aca acc aag atc act ctc aac	1361																				
Phe Leu Ser Glu Ser Gln Arg Gly Glu Thr Thr Lys Ile Thr Leu Asn																					
	310										315					320					
tgt gga aat cta ttc ttg cgg aac tta cat ccc acc agt gat caa gag	1409																				
Cys Gly Asn Leu Phe Leu Arg Asn Leu His Pro Thr Ser Asp Gln Glu																					
	325										330					335					
cca cag aga tta tgg aca ctt tgt tgc tta ctc cca aga aag ggc cag	1457																				
Pro Gln Arg Leu Trp Thr Leu Cys Cys Leu Leu Pro Arg Lys Gly Gln																					
	340										345					350					
cac cgt att tat ggc cag tgc tagaagggtcc tcaactgaagg caacagggaa	1508																				
His Arg Ile Tyr Gly Gln Cys																					
	355										360										
gaggcagcca tgaatatata cttggaaaca ggatcatttg aggccttcaa gaaggcataa	1568																				
aatattgtcc ctttcagcct ttcttttctt ctcaatgccca cgattaccaaa ttatgtttta	1628																				
atcttaagtg gctagtgtta tatgtgatac attatgcctt tgatatgtgg ttgaaaaaat	1688																				
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<210> 38
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<212> PRT
<213> Homo sapiens
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<210> 39  
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 <212> DNA  
 <213> Homo sapiens

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 Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu  
 1 5 10  
 ggc gcg gct cta gcc ggc ccg gtc ctt gga ctg aaa gaa tgc acc agg 161  
 Gly Ala Ala Leu Ala Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg  
 15 20 25  
 ggc tcg gca gtg tgg tgc cag aat gtg aag acg gcg tcc gac tgc ggg 209  
 Gly Ser Ala Val Trp Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly  
 30 35 40  
 gca gtg aag cac tgc ctg cag acc gtt tgg aac aag cca aca gtg aaa 257  
 Ala Val Lys His Cys Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys  
 45 50 55  
 tcc ctt ccc tgc gac ata tgc aaa gac gtt gtc acc gca gct ggt gat 305  
 Ser Leu Pro Cys Asp Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp  
 60 65 70 75  
 atg ctg aag gac aat gcc act gag gag gag atc ctt gtt tac ttg gag 353  
 Met Leu Lys Asp Asn Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu  
 80 85 90  
 aag acc tgt gac tgg ctt ccg aaa ccg aac atg tct gct tca tgc aag 401  
 Lys Thr Cys Asp Trp Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys  
 95 100 105  
 gag ata gtg gac tcc tac ctc cct gtc atc ctg gac atc att aaa gga 449  
 Glu Ile Val Asp Ser Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly  
 110 115 120  
 gaa atg agc cgt cct ggg gag gtg tgc tct gct ctc aac ctc tgc gag 497  
 Glu Met Ser Arg Pro Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu  
 125 130 135

tct ctc cag aag cac cta gca gag ctg aat cac cag aag cag ctg gag	545
Ser Leu Gln Lys His Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu	
140 145 150 155	
tcc aat aag atc cca gag ctg gac atg act gag gtg gtg gcc ccc ttc	593
Ser Asn Lys Ile Pro Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe	
160 165 170	
atg gcc aac atc cct ctc ctc ctc tac cct cag gac ggc ccc cgc agc	641
Met Ala Asn Ile Pro Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser	
175 180 185	
aag ccc cag cca aag gat aat ggg gac gtt tgc cag gac tgc att cag	689
Lys Pro Gln Pro Lys Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln	
190 195 200	
atg gtg act gac atc cag act gct gta cgg acc aac tcc acc ttt gtc	737
Met Val Thr Asp Ile Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val	
205 210 215	
cag gcc ttg gtg gaa cat gtc aag gag gag tgt gac cgc ctg ggc cct	785
Gln Ala Leu Val Glu His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro	
220 225 230 235	
ggc atg gcc gac ata tgc aag aac tat atc agc cag tat tct gaa att	833
Gly Met Ala Asp Ile Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile	
240 245 250	
gct atc cag atg atg atg cac atg cag gat cag caa ccc aag gag atc	881
Ala Ile Gln Met Met Met His Met Gln Asp Gln Gln Pro Lys Glu Ile	
255 260 265	
tgt gcg ctg gtt ggg ttc tgt gat gag gtg aaa gag atg ccc atg cag	929
Cys Ala Leu Val Gly Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln	
270 275 280	
act ctg gtc ccc gcc aaa gtg gcc tcc aag aat gtc atc cct gcc ctg	977
Thr Leu Val Pro Ala Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu	
285 290 295	
gaa ctg gtg gag ccc att aag aag cac gag gtc cca gca aag tct gat	1025
Glu Leu Val Glu Pro Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp	
300 305 310 315	
gtt tac tgt gag gtg tgt gaa ttc ctg gtg aag gag gtg acc aag ctg	1073
Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu	
320 325 330	
att gac aac aac aag act gag aaa gaa ata ctc gac gct ttt gac aaa	1121
Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys	
335 340 345	
atg tgc tcg aag ctg ccg aag tcc ctg tcg gaa gag tgc cag gag gtg	1169
Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val	
350 355 360	
gtg gac acg tac ggc agc tcc atc ctg tcc atc ctg ctg gag gag gtc	1217
Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val	
365 370 375	
agc cct gag ctg gtg tgc agc atg ctg cac ctc tgc tct ggc acg cgg	1265
Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg	
380 385 390 395	
ctg cct gca ctg acc gtt cac gtg act cag cca aag gac ggt ggc ttc	1313
Leu Pro Ala Leu Thr Val His Val Thr Gln Pro Lys Asp Gly Gly Phe	
400 405 410	
tgc gaa gtg tgc aag aag ctg gtg ggt tat ttg gat cgc aac ctg gag	1361
Cys Glu Val Cys Lys Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu	
415 420 425	

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<211> 479
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<213> Homo sapiens
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			20					25					30		
Cys	Gln	Asn	Val	Lys	Thr	Ala	Ser	Asp	Cys	Gly	Ala	Val	Lys	His	Cys
		35					40					45			
Leu	Gln	Thr	Val	Trp	Asn	Lys	Pro	Thr	Val	Lys	Ser	Leu	Pro	Cys	Asp
	50					55					60				
Ile	Cys	Lys	Asp	Val	Val	Thr	Ala	Ala	Gly	Asp	Met	Leu	Lys	Asp	Asn
65					70					75				80	
Ala	Thr	Glu	Glu	Glu	Ile	Leu	Val	Tyr	Leu	Glu	Lys	Thr	Cys	Asp	Trp
				85					90					95	
Leu	Pro	Lys	Pro	Asn	Met	Ser	Ala	Ser	Cys	Lys	Glu	Ile	Val	Asp	Ser
			100					105					110		

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Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
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    130                      135                      140
Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
145                      150                      155                      160
Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
    165                      170                      175
Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
    180                      185                      190
Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile
    195                      200                      205
Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu
    210                      215                      220
His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile
225                      230                      235                      240
Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met
    245                      250                      255
Met His Met Gln Asp Gln Gln Pro Lys Glu Ile Cys Ala Leu Val Gly
    260                      265                      270
Phe Cys Asp Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala
    275                      280                      285
Lys Val Ala Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro
    290                      295                      300
Ile Lys Lys His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val
305                      310                      315                      320
Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
    325                      330                      335
Thr Glu Lys Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu
    340                      345                      350
Pro Lys Ser Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly
    355                      360                      365
Ser Ser Ile Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val
    370                      375                      380
Cys Ser Met Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr
385                      390                      395                      400
Val His Val Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys
    405                      410                      415
Lys Leu Val Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys
    420                      425                      430
Gln Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp
    435                      440                      445
Pro Tyr Gln Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val
    450                      455                      460
Leu Ile Glu Ile Leu Val Glu Val Trp Ile Leu Pro Ser Cys Ala
465                      470                      475

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<210> 41

<211> 770

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..120

<220>

<221> CDS

<222> 121..546

<220>

<221> 3'UTR

<222> 547..770

<220>

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<222> 739..744

<220>

<221> polyA\_site

<222> 755..770

<400> 41

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caagagtctg atcagcagcc tcttcctcct ccaggaccca gaagccctga gcttatcccc 120
atg gag ctc tgc cgg tcc ctg gcc ctg ctg ggg ggc tcc ctg ggc ctg 168
Met Glu Leu Cys Arg Ser Leu Ala Leu Leu Gly Gly Ser Leu Gly Leu
-35 -30 -25
atg ttc tgc ctg att gct ttg agc acc gat ttc tgg ttt gag gct gtg 216
Met Phe Cys Leu Ile Ala Leu Ser Thr Asp Phe Trp Phe Glu Ala Val
-20 -15 -10
ggg ccc acc cac tca gct cac tcg ggc ctc tgg cca aca ggg cat ggg 264
Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly
-5 1 5 10
gac atc ata tca ggc cac ggc ccg ctt gtc tca acc acc gca gcc ttt 312
Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe
15 20 25
gct gca ggt aag gac tct gga ctg gac tgg ggc atc gcg agc cag cga 360
Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg
30 35 40
att cct gcc gag gag ctg agc cat ctc tct tgt cct tgt ccc cag cca 408
Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro
45 50 55
tct cca tgg tgg tgg cca tgg cgg tgt aca cca gcg agc ggt ggg acc 456
Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr
60 65 70 75
agc ctc cac acc ccc aga tcc aga cct tct tct cct ggt cct tct acc 504
Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr
80 85 90
tgg gct ggg tct cag cta tcc tct tgc tct gta cag gtg ccc 546
Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro
95 100 105
tgagcctggg tgctcactgt ggcgggtcccc gtccctggcta tgaaaccttg tgagcagaag 606
gcaagagcgg caagatgagtt tttgagcgtt gtattccaaa ggcctcatct ggagcctcgg 666
gaaagtctgg tcccacatct gcccgccctt ccagcccttc cccagccctt cctcttggtt 726
cttcattcat tcaacaaaat ttggctggaa aaaaaaaaaa aaaa 770

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<210> 42

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 <213> Homo sapiens

<220>  
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 <222> 1..37

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 Gly Pro Thr His Ser Ala His Ser Gly Leu Trp Pro Thr Gly His Gly  
           -5                          1                          5                          10  
 Asp Ile Ile Ser Gly His Gly Pro Leu Val Ser Thr Thr Ala Ala Phe  
                           15                          20                          25  
 Ala Ala Gly Lys Asp Ser Gly Leu Asp Trp Gly Ile Ala Ser Gln Arg  
                           30                          35                          40  
 Ile Pro Ala Glu Glu Leu Ser His Leu Ser Cys Pro Cys Pro Gln Pro  
           45                          50                          55  
 Ser Pro Trp Trp Trp Pro Trp Arg Cys Thr Pro Ala Ser Gly Gly Thr  
           60                          65                          70                          75  
 Ser Leu His Thr Pro Arg Ser Arg Pro Ser Ser Pro Gly Pro Ser Thr  
                           80                          85                          90  
 Trp Ala Gly Ser Gln Leu Ser Ser Cys Ser Val Gln Val Pro  
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<220>  
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 <222> 1255..1340

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cccactagg	tgaag	atg	tca	gcc	cag	gag	agc	tgc	ctc	agc	ctc	atc	aag	171		
	Met	Ser	Ala	Gln	Glu	Ser	Cys	Leu	Ser	Leu	Ile	Lys				
	1				5					10						
tac	ttc	ctc	ttc	gtt	ttc	aac	ctc	ttc	ttc	ttc	gtc	ctc	ggc	agc	ctg	219
Tyr	Phe	Leu	Phe	Val	Phe	Asn	Leu	Phe	Phe	Phe	Val	Leu	Gly	Ser	Leu	
	15					20					25					
atc	ttc	tgc	ttc	ggc	atc	tgg	atc	ctc	att	gac	aag	acc	agc	ttc	gtg	267
Ile	Phe	Cys	Phe	Gly	Ile	Trp	Ile	Leu	Ile	Asp	Lys	Thr	Ser	Phe	Val	
	30					35					40					
tcc	ttt	gtg	ggc	ttg	gcc	ttc	gtg	cct	ctg	cag	atc	tgg	tcc	aaa	gtc	315
Ser	Phe	Val	Gly	Leu	Ala	Phe	Val	Pro	Leu	Gln	Ile	Trp	Ser	Lys	Val	
45					50					55					60	
ctg	gcc	atc	tca	gga	atc	ttc	acc	atg	ggc	atc	gcc	ctc	ctg	ggt	tgt	363
Leu	Ala	Ile	Ser	Gly	Ile	Phe	Thr	Met	Gly	Ile	Ala	Leu	Leu	Gly	Cys	
				65					70					75		
gtg	ggg	gcc	ctc	aag	gag	ctc	cgc	tgc	ctc	ctg	ggc	ctg	tat	ttt	ggg	411
Val	Gly	Ala	Leu	Lys	Glu	Leu	Arg	Cys	Leu	Leu	Gly	Leu	Tyr	Phe	Gly	
			80					85					90			
atg	ctg	ctg	ctc	ctg	ttt	gcc	aca	cag	atc	acc	ctg	gga	atc	ctc	atc	459
Met	Leu	Leu	Leu	Leu	Phe	Ala	Thr	Gln	Ile	Thr	Leu	Gly	Ile	Leu	Ile	
			95					100					105			
tcc	act	cag	cgg	gcc	agc	tgg	agc	gaa	gct	tgc	ggg	acg	tcg			501
Ser	Thr	Gln	Arg	Ala	Ser	Trp	Ser	Glu	Ala	Cys	Gly	Thr	Ser			
			110					115					120			
tagagaaaac	catccaaaag	tacggcacca	accccagagga	gaccgcgggc	gaggagagct	561										
gggactatgt	gcagttccag	ctgcgctgct	gcggctggca	ctaccgcgag	gactggttcc	621										
aagtctcat	cctgagaggt	aacgggtcgg	aggcgcaccg	cgtgccctgc	tcctgctaca	681										
acttgctggc	gaccaacgac	tccacaatcc	tagataaggt	gatcttgccc	cagctcagca	741										
ggcttggaca	cctggcgcg	tccagacaca	gtgcagacat	ctgcgctgtc	cctgcagaga	801										
gccacatcta	ccgcgagggc	tgcgcgcagg	gcctccagaa	gtggctgcac	aacaacctta	861										
tttccatagt	gggcatttgc	ctgggcgtcg	gcctactcga	gctcgggttc	atgacgctct	921										
cgatattcct	gtgcagaaac	ctggaccacg	tctacaaccg	gctcgctcga	taccgttagg	981										
ccccgccctc	cccaaagtcc	cgccccgccc	ccgtcacgtg	cgtcgggcac	ttccctgctg	1041										
cctgtaaata	tttgtttaat	cccagttcg	cctggagccc	tcctccttca	cattcccctg	1101										
gggacccacg	tggctgcgtg	ccctgctgc	tgtcacctct	cccacggagc	ctggggcttt	1161										
cgtccacagc	ttctgtctcc	catctgtcgg	cctaccacca	cccacaagat	tatttttcac	1221										
ccaaacctca	aataaaatccc	ctgcgttttt	ggtaaaaaaaaa	aaaaaaaaaaaa	aaaaaaaaaaaa	1281										
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<210> 44
<211> 122
<212> PRT
<213> Homo sapiens
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			20					25					30		
Gly	Ile	Trp	Ile	Leu	Ile	Asp	Lys	Thr	Ser	Phe	Val	Ser	Phe	Val	Gly
		35					40					45			
Leu	Ala	Phe	Val	Pro	Leu	Gln	Ile	Trp	Ser	Lys	Val	Leu	Ala	Ile	Ser



50		55		60
Gly Ile Phe Thr Met	Gly Ile Ala Leu Leu	Gly Cys Val Gly Ala Leu		
65	70	75	80	
Lys Glu Leu Arg Cys	Leu Leu Gly Leu Tyr Phe	Gly Met Leu Leu Leu		
	85	90	95	
Leu Phe Ala Thr Gln	Ile Thr Leu Gly Ile	Leu Ile Ser Thr Gln Arg		
	100	105	110	
Ala Ser Trp Ser Glu	Ala Cys Gly Thr Ser			
115	120			

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 <212> DNA  
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<220>  
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<220>  
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 <222> 1956..1999

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 atg cgc ctc cgc cgc cta gcg ctg ttc ccg ggt gtg gcg ctg ctt ctt 165  
 Met Arg Leu Arg Arg Leu Ala Leu Phe Pro Gly Val Ala Leu Leu Leu  
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 gcc gcg gcc cgc ctc gcc gct gcc tcc gac gtg cta gaa ctc acg gac 213  
 Ala Ala Ala Arg Leu Ala Ala Ala Ser Asp Val Leu Glu Leu Thr Asp  
 -5 1 5  
 gac aac ttc gag agt cgc atc tcc gac acg ggc tct gcg ggc ctc atg 261  
 Asp Asn Phe Glu Ser Arg Ile Ser Asp Thr Gly Ser Ala Gly Leu Met  
 10 15 20  
 ctc gtc gag ttc ttc gct ccc tgg tgt gga cac tgc aag aga ctt gca 309  
 Leu Val Glu Phe Phe Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala  
 25 30 35 40  
 cct gag tat gaa gct gca gct acc aga tta aaa gga ata gtc cca tta 357  
 Pro Glu Tyr Glu Ala Ala Ala Thr Arg Leu Lys Gly Ile Val Pro Leu  
 45 50 55  
 gca aag gtt gat tgc act gcc aac act aac acc tgt aat aaa tat gga 405

Ala	Lys	Val	Asp 60	Cys	Thr	Ala	Asn 65	Thr	Asn	Thr	Cys	Asn	Lys 70	Tyr	Gly	
gtc	agt	gga	tat	cca	acc	ctg	aag	ata	ttt	aga	gat	ggg	gaa	gaa	gca	453
Val	Ser	Gly	Tyr	Pro	Thr	Leu	Lys	Ile	Phe	Arg	Asp	Gly	Glu	Glu	Ala	
		75					80					85				
ggg	gct	tat	gat	gga	cct	agg	act	gct	gat	gga	att	gtc	agc	cac	ttg	501
Gly	Ala	Tyr	Asp	Gly	Pro	Arg	Thr	Ala	Asp	Gly	Ile	Val	Ser	His	Leu	
		90					95				100					
aag	aag	cag	gca	gga	cca	gct	tca	gtg	cct	ctc	agg	act	gag	gaa	gaa	549
Lys	Lys	Gln	Ala	Gly	Pro	Ala	Ser	Val	Pro	Leu	Arg	Thr	Glu	Glu	Glu	
105					110						115				120	
ttt	aag	aaa	ttc	att	agt	gat	aaa	gat	gcc	tct	ata	gta	ggg	ttt	ttc	597
Phe	Lys	Lys	Phe	Ile	Ser	Asp	Lys	Asp	Ala	Ser	Ile	Val	Gly	Phe	Phe	
			125						130					135		
gat	gat	tca	ttc	agt	gag	gct	cac	tcc	gag	ttc	cta	aaa	gca	gcc	agc	645
Asp	Asp	Ser	Phe	Ser	Glu	Ala	His	Ser	Glu	Phe	Leu	Lys	Ala	Ala	Ser	
			140						145					150		
aac	ttg	agg	gat	aac	tac	cga	ttt	gca	cat	acg	aat	gtt	gag	tct	ctg	693
Asn	Leu	Arg	Asp	Asn	Tyr	Arg	Phe	Ala	His	Thr	Asn	Val	Glu	Ser	Leu	
		155					160					165				
gtg	aac	gag	tat	gat	gat	aat	gga	gag	ggg	atc	atc	tta	ttt	cgt	cct	741
Val	Asn	Glu	Tyr	Asp	Asp	Asn	Gly	Glu	Gly	Ile	Ile	Leu	Phe	Arg	Pro	
		170					175				180					
tca	cat	ctc	act	aac	aag	ttt	gag	gac	aag	act	gtg	gca	tat	aca	gag	789
Ser	His	Leu	Thr	Asn	Lys	Phe	Glu	Asp	Lys	Thr	Val	Ala	Tyr	Thr	Glu	
185					190					195					200	
caa	aaa	atg	acc	agt	ggc	aaa	att	aaa	aag	ttt	atc	cag	gaa	aac	att	837
Gln	Lys	Met	Thr	Ser	Gly	Lys	Ile	Lys	Lys	Phe	Ile	Gln	Glu	Asn	Ile	
			205						210					215		
ttt	ggg	atc	tgc	cct	cac	atg	aca	gaa	gac	aat	aaa	gat	ttg	ata	cag	885
Phe	Gly	Ile	Cys	Pro	His	Met	Thr	Glu	Asp	Asn	Lys	Asp	Leu	Ile	Gln	
			220						225				230			
ggc	aag	gac	tta	ctt	att	gct	tac	tat	gat	gtg	gac	tat	gaa	aag	aac	933
Gly	Lys	Asp	Leu	Leu	Ile	Ala	Tyr	Tyr	Asp	Val	Asp	Tyr	Glu	Lys	Asn	
		235					240					245				
gct	aaa	ggg	tcc	aac	tac	agg	aga	aac	agg	gta	atg	atg	gtg	gca	aag	981
Ala	Lys	Gly	Ser	Asn	Tyr	Arg	Arg	Asn	Arg	Val	Met	Met	Val	Ala	Lys	
		250					255				260					
aaa	ttc	ctg	gat	gct	ggg	cac	aaa	ctc	aac	ttt	gct	gta	gct	agc	cgc	1029
Lys	Phe	Leu	Asp	Ala	Gly	His	Lys	Leu	Asn	Phe	Ala	Val	Ala	Ser	Arg	
265					270					275					280	
aaa	acc	ttt	agc	cat	gaa	ctt	tct	gat	ttt	ggc	ttg	gag	agc	act	gct	1077
Lys	Thr	Phe	Ser	His	Glu	Leu	Ser	Asp	Phe	Gly	Leu	Glu	Ser	Thr	Ala	
			285						290					295		
gga	gag	att	cct	gtt	gtt	gct	atc	aga	act	gct	aaa	gga	gag	aag	ttt	1125
Gly	Glu	Ile	Pro	Val	Val	Ala	Ile	Arg	Thr	Ala	Lys	Gly	Glu	Lys	Phe	
			300					305				310				
gtc	atg	cag	gag	gag	ttc	tcg	cgt	gat	ggg	aag	gct	ctg	gag	agg	ttc	1173
Val	Met	Gln	Glu	Glu	Phe	Ser	Arg	Asp	Gly	Lys	Ala	Leu	Glu	Arg	Phe	
		315					320					325				
ctg	cag	gat	tac	ttt	gat	ggc	aat	ctg	aag	aga	tac	ctg	aag	tct	gaa	1221
Leu	Gln	Asp	Tyr	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Tyr	Leu	Lys	Ser	Glu	
		330				335					340					
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<213> Homo sapiens
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<222> 1..24
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Asp	Asn	Phe	Glu	Ser	Arg	Ile	Ser	Asp	Thr	Gly	Ser	Ala	Gly	Leu	Met	
	10					15					20					
Leu	Val	Glu	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Arg	Leu	Ala	
25					30					35					40	
Pro	Glu	Tyr	Glu	Ala	Ala	Ala	Thr	Arg	Leu	Lys	Gly	Ile	Val	Pro	Leu	
				45					50					55		
Ala	Lys	Val	Asp	Cys	Thr	Ala	Asn	Thr	Asn	Thr	Cys	Asn	Lys	Tyr	Gly	

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Val	Ser	Gly	Tyr	Pro	Thr	Leu	Lys	Ile	Phe	Arg	Asp	Gly	Glu	Glu	Ala
		75					80					85			
Gly	Ala	Tyr	Asp	Gly	Pro	Arg	Thr	Ala	Asp	Gly	Ile	Val	Ser	His	Leu
	90					95					100				
Lys	Lys	Gln	Ala	Gly	Pro	Ala	Ser	Val	Pro	Leu	Arg	Thr	Glu	Glu	Glu
105					110					115					120
Phe	Lys	Lys	Phe	Ile	Ser	Asp	Lys	Asp	Ala	Ser	Ile	Val	Gly	Phe	Phe
				125					130					135	
Asp	Asp	Ser	Phe	Ser	Glu	Ala	His	Ser	Glu	Phe	Leu	Lys	Ala	Ala	Ser
			140					145					150		
Asn	Leu	Arg	Asp	Asn	Tyr	Arg	Phe	Ala	His	Thr	Asn	Val	Glu	Ser	Leu
		155					160					165			
Val	Asn	Glu	Tyr	Asp	Asp	Asn	Gly	Glu	Gly	Ile	Ile	Leu	Phe	Arg	Pro
	170					175					180				
Ser	His	Leu	Thr	Asn	Lys	Phe	Glu	Asp	Lys	Thr	Val	Ala	Tyr	Thr	Glu
185					190					195					200
Gln	Lys	Met	Thr	Ser	Gly	Lys	Ile	Lys	Lys	Phe	Ile	Gln	Glu	Asn	Ile
				205					210					215	
Phe	Gly	Ile	Cys	Pro	His	Met	Thr	Glu	Asp	Asn	Lys	Asp	Leu	Ile	Gln
			220					225					230		
Gly	Lys	Asp	Leu	Leu	Ile	Ala	Tyr	Tyr	Asp	Val	Asp	Tyr	Glu	Lys	Asn
		235					240					245			
Ala	Lys	Gly	Ser	Asn	Tyr	Arg	Arg	Asn	Arg	Val	Met	Met	Val	Ala	Lys
	250					255					260				
Lys	Phe	Leu	Asp	Ala	Gly	His	Lys	Leu	Asn	Phe	Ala	Val	Ala	Ser	Arg
265					270					275					280
Lys	Thr	Phe	Ser	His	Glu	Leu	Ser	Asp	Phe	Gly	Leu	Glu	Ser	Thr	Ala
				285					290					295	
Gly	Glu	Ile	Pro	Val	Val	Ala	Ile	Arg	Thr	Ala	Lys	Gly	Glu	Lys	Phe
			300					305					310		
Val	Met	Gln	Glu	Glu	Phe	Ser	Arg	Asp	Gly	Lys	Ala	Leu	Glu	Arg	Phe
		315					320					325			
Leu	Gln	Asp	Tyr	Phe	Asp	Gly	Asn	Leu	Lys	Arg	Tyr	Leu	Lys	Ser	Glu
	330					335					340				
Pro	Ile	Pro	Glu	Ser	Asn	Asp	Gly	Pro	Val	Lys	Val	Val	Val	Ala	Glu
345					350					355					360
Asn	Phe	Asp	Glu	Ile	Val	Asn	Asn	Glu	Asn	Lys	Asp	Val	Leu	Ile	Glu
				365						370				375	
Phe	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Asn	Leu	Glu	Pro	Lys	Tyr
			380					385					390		
Lys	Glu	Leu	Gly	Glu	Lys	Leu	Ser	Lys	Asp	Pro	Asn	Ile	Val	Ile	Ala
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 <212> DNA  
 <213> Homo sapiens

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<220>  
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<220>  
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 <222> 722..836

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 gatgctgtgg ttggatattt agaggacatt atc atg gat gac gag ttc cag tta 174  
 Met Asp Asp Glu Phe Gln Leu  
 1 5  
 tta cag aga aat ttc atg gac aag tac tac ctg gag ttt gaa gac aca 222  
 Leu Gln Arg Asn Phe Met Asp Lys Tyr Tyr Leu Glu Phe Glu Asp Thr  
 10 15 20  
 gaa gag aat aaa ctc atc tac aca cct att ttt aat gaa tac att tct 270  
 Glu Glu Asn Lys Leu Ile Tyr Thr Pro Ile Phe Asn Glu Tyr Ile Ser  
 25 30 35  
 ttg gta gaa aaa tac att gaa gaa cag ctg ctg cag cgg att cct gag 318  
 Leu Val Glu Lys Tyr Ile Glu Glu Gln Leu Leu Gln Arg Ile Pro Glu  
 40 45 50 55  
 ttc aac atg gca gcc ttc acc aca aca tta cag cac cat aag gat gaa 366  
 Phe Asn Met Ala Ala Phe Thr Thr Thr Leu Gln His His Lys Asp Glu  
 60 65 70  
 gtg gct ggt gac ata ttc gac atg ctg ctc acc ttc aca gat ttt ctg 414  
 Val Ala Gly Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu  
 75 80 85  
 gct ttt aaa gaa atg ttt ttg gac tac aga gca gaa aaa gaa ggc cga 462  
 Ala Phe Lys Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg  
 90 95 100  
 gga ctg gac tta agc agt ggc tta gtg gtg act tca ttg tgc aaa tca 510  
 Gly Leu Asp Leu Ser Ser Gly Leu Val Val Thr Ser Leu Cys Lys Ser  
 105 110 115  
 tct tct ctg cca gct tcc cag aac aat ctg cgg cac taggtcctac 556  
 Ser Ser Leu Pro Ala Ser Gln Asn Asn Leu Arg His  
 120 125 130  
 ctccagccaa tgaatgggat cattctggat gtcaccagcc caataggctc agctcatgat 616  
 gacagaacac atcttggaaa gactgactct gttatgtaac tcttcattta tgttaagtat 676  
 taataggtca aaacccaaat gacctaacc tcttgacct atttcaaaaa aaaaaaaaaa 736

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 <213> Homo sapiens

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 Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln  
 35 40 45  
 Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr  
 50 55 60  
 Leu Gln His His Lys Asp Glu Val Ala Gly Asp Ile Phe Asp Met Leu  
 65 70 75 80  
 Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys Glu Met Phe Leu Asp Tyr  
 85 90 95  
 Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp Leu Ser Ser Gly Leu Val  
 100 105 110  
 Val Thr Ser Leu Cys Lys Ser Ser Ser Leu Pro Ala Ser Gln Asn Asn  
 115 120 125  
 Leu Arg His  
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 tctcctgccc cctcctgtct cgtaaataac ttttttactc taaagaaaga aagacaaaag 180  
 tagtcgtccg ccccc atg cat ccc ttc tac acc cgg gcc gcc acc atg ata 231

	Met	His	Pro	Phe	Tyr	Thr	Arg	Ala	Ala	Thr	Met	Ile	
	1				5					10			
ggc gag atc gcc gcc gcc gtg tcc ttc atc tcc aag ttt ctc cgc acc													279
Gly Glu Ile Ala Ala Ala Val Ser Phe Ile Ser Lys Phe Leu Arg Thr													
	15				20					25			
aag ggg ctc acg agc gag cga cag ctg cag acc ttc agc cag agc ctg													327
Lys Gly Leu Thr Ser Glu Arg Gln Leu Gln Thr Phe Ser Gln Ser Leu													
	30				35					40			
cag gag ctg ctg gca gaa cat tat aaa cat cac tgg ttc cca gaa aag													375
Gln Glu Leu Leu Ala Glu His Tyr Lys His His Trp Phe Pro Glu Lys													
	45				50					55			60
cca tgc aag gga tgc ggt tac cgt tgt att cgc atc aac cat aaa atg													423
Pro Cys Lys Gly Ser Gly Tyr Arg Cys Ile Arg Ile Asn His Lys Met													
	65				70					75			
gat cct ctg att gga cag gca gca cag cgg att gga ctg agc agt cag													471
Asp Pro Leu Ile Gly Gln Ala Ala Gln Arg Ile Gly Leu Ser Ser Gln													
	80				85					90			
gag ctg ttc agg ctt ctc cca agt gaa ctc aca ctc tgg gtt gac ccc													519
Glu Leu Phe Arg Leu Leu Pro Ser Glu Leu Thr Leu Trp Val Asp Pro													
	95				100					105			
tat gaa gtg tcc tac aga att gga gag gat ggc tcc atc tgt gtg ctg													567
Tyr Glu Val Ser Tyr Arg Ile Gly Glu Asp Gly Ser Ile Cys Val Leu													
	110				115					120			
tat gaa gcc tca cca gca gga ggt agc act caa aac agc acc aac gtg													615
Tyr Glu Ala Ser Pro Ala Gly Gly Ser Thr Gln Asn Ser Thr Asn Val													
	125				130					135			140
caa atg gta gac agc cga atc agc tgt aag gag gaa ctt ctc ttg ggc													663
Gln Met Val Asp Ser Arg Ile Ser Cys Lys Glu Glu Leu Leu Leu Gly													
	145				150					155			
aga acg agc cct tcc aaa aac tac aat atg atg act gta tca agt													708
Arg Thr Ser Pro Ser Lys Asn Tyr Asn Met Met Thr Val Ser Ser													
	160				165					170			
taagatatag tctgtggatg gatcatctga tgaatgatgga taaatttgat ttttgctttg													768
ggtagggctcc tcttggggat ggattatgga atttaaacca tgtcacagct gtgaagatct													828
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<211> 171

<212> PRT

<213> Homo sapiens

<400> 50

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Ala	Ala	Val	Ser	Phe	Ile	Ser	Lys	Phe	Leu	Arg	Thr	Lys	Gly	Leu	Thr
		20					25					30			
Ser	Glu	Arg	Gln	Leu	Gln	Thr	Phe	Ser	Gln	Ser	Leu	Gln	Glu	Leu	Leu
		35				40						45			
Ala	Glu	His	Tyr	Lys	His	His	Trp	Phe	Pro	Glu	Lys	Pro	Cys	Lys	Gly
	50					55				60					
Ser	Gly	Tyr	Arg	Cys	Ile	Arg	Ile	Asn	His	Lys	Met	Asp	Pro	Leu	Ile
	65				70				75					80	
Gly	Gln	Ala	Ala	Gln	Arg	Ile	Gly	Leu	Ser	Ser	Gln	Glu	Leu	Phe	Arg
				85				90						95	





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Leu Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala
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Val Leu Arg Gln Asp Gly Val Val Val Thr Ile Asn Lys Lys Arg Asn
          80          85          90
ctg gtg gtg tct gtg gac gac ggt ggc acc ttt gag gtt gtt ttg cac 445
Leu Val Val Ser Val Asp Asp Gly Gly Thr Phe Glu Val Val Leu His
          95          100          105
cga gtg tgg aag ggg agc tcg gtc cac cag gac ttc ctg ggc ttc tat 493
Arg Val Trp Lys Gly Ser Ser Val His Gln Asp Phe Leu Gly Phe Tyr
          110          115          120
gtg ctg gac agt cat cgg atg tca gcc cgg acg cac ggg ctg ctg ggg 541
Val Leu Asp Ser His Arg Met Ser Ala Arg Thr His Gly Leu Leu Gly
          125          130          135
caa ttt ttc cac ccc atc ggt ttt gaa gtg tct gac atc cac cca ggc 589
Gln Phe Phe His Pro Ile Gly Phe Glu Val Ser Asp Ile His Pro Gly
          140          145          150
tct gac ccc aca aag cca gat gcc acg atg gtg gtg agg aac cgc cgg 637
Ser Asp Pro Thr Lys Pro Asp Ala Thr Met Val Val Arg Asn Arg Arg
          160          165          170
ctc acg gtc acc agg ggt ttg caa aaa gac tac agc aag gac ccg tgg 685
Leu Thr Val Thr Arg Gly Leu Gln Lys Asp Tyr Ser Lys Asp Pro Trp
          175          180          185
cat ggg gcc gag gtg tcc tgc tgg ttc att cac aac aat ggg gct gga 733
His Gly Ala Glu Val Ser Cys Trp Phe Ile His Asn Asn Gly Ala Gly
          190          195          200
ctc atc gat ggt gcc tac act gat tat atc gtc ccc gac atc ttc 778
Leu Ile Asp Gly Ala Tyr Thr Asp Tyr Ile Val Pro Asp Ile Phe
          205          210          215
tgagccctct ggccagcacg cctgtcctcc cccggggcca aggcagagga ggaggacgac 838
atcctgacct gctgctgagg ctgtacctcc ttgactaagc tggttccttg tgtcaaagca 898
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-5          1          5          10
Thr Gly Gly Phe Ser Val Asn Gly Gln Leu Ile Gly Asn Lys Ala Arg
          15          20          25
Ser Pro Gly Gln His Asp Gly Thr Tyr Phe Gly Arg Leu Gly Ile Ala
          30          35          40
Asn Pro Ala Thr Asp Phe Gln Leu Glu Val Thr Pro Gln Asn Ile Thr
          45          50          55
Leu Asn Pro Gly Phe Gly Gly Pro Val Phe Ser Trp Arg Asp Gln Ala

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60					65					70					75
Val	Leu	Arg	Gln	Asp	Gly	Val	Val	Val	Thr	Ile	Asn	Lys	Lys	Arg	Asn
				80					85					90	
Leu	Val	Val	Ser	Val	Asp	Asp	Gly	Gly	Thr	Phe	Glu	Val	Val	Leu	His
			95				100						105		
Arg	Val	Trp	Lys	Gly	Ser	Ser	Val	His	Gln	Asp	Phe	Leu	Gly	Phe	Tyr
		110					115					120			
Val	Leu	Asp	Ser	His	Arg	Met	Ser	Ala	Arg	Thr	His	Gly	Leu	Leu	Gly
	125					130					135				
Gln	Phe	Phe	His	Pro	Ile	Gly	Phe	Glu	Val	Ser	Asp	Ile	His	Pro	Gly
140					145					150					155
Ser	Asp	Pro	Thr	Lys	Pro	Asp	Ala	Thr	Met	Val	Val	Arg	Asn	Arg	Arg
				160					165					170	
Leu	Thr	Val	Thr	Arg	Gly	Leu	Gln	Lys	Asp	Tyr	Ser	Lys	Asp	Pro	Trp
			175					180					185		
His	Gly	Ala	Glu	Val	Ser	Cys	Trp	Phe	Ile	His	Asn	Asn	Gly	Ala	Gly
	190						195					200			
Leu	Ile	Asp	Gly	Ala	Tyr	Thr	Asp	Tyr	Ile	Val	Pro	Asp	Ile	Phe	
	205					210					215				